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A new coastal rock-dwelling gecko of the subgenus *Japonigekko* (Squamata, Gekkonidae, *Gekko*) from western Kyushu, Japan

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Abstract

A remarkable new species of the subgenus *Japonigekko* from the islands of Gotō Nada and offshore islands of Kagoshima Prefecture, Kyushu, Japan, inhabiting rocky coastal habitats, is described based on morphological characters and molecular evidence. Morphologically, *Gekko* (*Japonigekko*) *asahi* **sp. nov.** can be distinguished from its congeners by its moderate body size; interorbital scales between anterior corners of eyes 34–44; dorsal tubercles large, strongly elevated, and arranged in 12–16 rows at midbody; 127–158 midbody scale rows; 32–45 ventral scale rows; 158–189 ventral scales between the mental and the cloacal slit; subdigital lamellae 8–11 on finger I, 9–14 on finger IV, 9–12 on toe I, and 10–18 on toe IV; webbing absent; 6–9 precloacal pores in males, and absent in females; one postcloacal tubercle on each side, with the midpoint of the tubercle distinctly concave in some male individuals; and its distinctive dorsal coloration. Phylogenetically, the new species represents a distinct clade within the subgenus *Japonigekko*, forming a sister group with *G. kaiyai* from Henan Province of China, and together they cluster with *G. hokouensis*. It differs from its congeners by uncorrected *p*-distances of at least 15.1% in *ND2* and 7.6% in *16S*. Currently, the new species is known only from low-elevation coastal rocky shores and building walls on island of Gotō Nada and Nishisonogi Peninsula, Nagasaki Prefecture and offshore islands of Kagoshima and Satsuma Peninsula, Kagoshima Prefecture, Japan. The discovery of this new species increases the total number of species in the subgenus *Japonigekko* to 40, of which seven species are distributed in Japan.

Key Words

Gekko asahi sp. nov., geographical isolation, Gotō Nada, morphology, molecular phylogeny, systematics

Introduction

The genus *Gekko* Laurenti, 1768, is the type genus of the family Gekkonidae Gray, 1825, comprising 94 currently recognized species (Uetz et al. 2025). These nocturnal reptiles typically inhabit walls, rocks, and trees, and are widely distributed across East and Southeast Asia, as well as parts of western Oceania and Melanesia (Cao et al. 2025, 2026; Huang et al. 2025; Pauwels et al. 2025; Xu et al. 2025). Within the genus, some species that occur in East Asia, particularly in China, Japan, Vietnam, and Laos, represent morphologically and phylogenetically distinct monophyletic lineages. Wood Jr et al. (2020) established a new subgenus, *Japonigekko* Wood, Guo, Travers, Su, Olson, Bauer, Grismer, Siler, Moyle, Andersen & Brown, to accommodate these species.

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The subgenus *Japonigekko* was phylogenetically defined as a maximum crown-clade name referring to the clade originating with the most recent common ancestor of *G. chinensis* (Gray, 1842) and *G. swinhonis* Günther, 1864 and including all extant species that share a more recent common ancestor with these species than with any of the type species of the other subgenera recognized in Wood Jr et al. (2020). Morphologically, members of the subgenus *Japonigekko* were characterized as relatively small to moderate-sized taxa (59–99 mm SVL) with the presence or absence of dorsal tubercle rows (up to 21 rows); possessing up to 32 precloacal pores (but most taxa lacking pores altogether); the absence of tubercles on ventrolateral folds; and the presence of some degree of interdigital webbing (from minimal to extensively webbed) (Wood Jr et al. 2020). More recently, Cao et al. (2026) provided a multilocus phylogeny and discussed diversity and historical biogeography of this subgenus; their analyses recovered at least nine candidate new species. Currently, the subgenus *Japonigekko* contains 39 nominal species, of which six species of the *Gekko* (*Japonigekko*) are known in Japan, including *G. japonicus* (Schlegel in Duméril & Bibron, 1836), *G. hokouensis* Pope, 1928, *G. tawaensis* Okada, 1956, *G. yakuensis* Matsui & Okada, 1968, *G. vertebralis* and *G. shibatai* Toda, Sengoku, Hikida & Ota, 2008 (Huang et al. 2025; Xu et al. 2025; Uetz et al. 2025).

The Gotō Islands are an archipelago of more than 140 islands and islets located between the Sea of Japan and the East China Sea, approximately 100 km from the mainland Kyushu. The archipelago has a rich natural environment with a complex coastline, including natural beaches, sea cliffs, and volcanic landscapes. Therefore, a wide variety of flora and fauna have been recorded on the archipelago, while the Ministry of the Environment of Japan has selected this area as one of the key ecologically and biologically significant marine areas in Japan (Ministry of the Environment of Japan 2025).

For a long period of time, the Gotō Islands were believed to be inhabited only by *Gekko japonicus* and *G. hokouensis* (Matsuo et al. 1988; Matsuo 2019; Chiba and Chiba 2024). However, Matsuo et al. (1988) reported an unidentified *Gekko* from Nakodori Island that belonged to neither of these species. To distinguish this lineage from other Japanese *Gekko*, Matsuo and Ejima (1988) provisionally referred to it as "Nishi-yamori" (Western Gecko) in Japanese, treating it as a cryptic species within the genus *Gekko*. This provisional name was subsequently used for many years in the official Red Lists of Nagasaki and Kagoshima Prefectures. Following the initial discovery, this gecko was later recorded not only from other islands of the Gotō archipelago, but also from Hirado Island, the Danjo Islands, the Koshiki Islands, the Uji Islands, the Kusagaki Islands, and from the western Kyushu mainland (Morita 1987, 1988; Matsuo and Ejima 1988, 1989a, 1989b; Tokunaga 1988; Sengoku 1989; Shibata 1990; Matsuo 2019) (Fig. 1; Suppl. material 1: table S1). Later, Shibata (1990) compared the coloration, numbers of precloacal pores and cloacal spurs of specimens from the Koshiki Islands with those of 23 *Gekko* species distributed across East and Southeast Asia, and found that they exhibited diagnostic traits distinct from all other known species. These specimens were identified as the same cryptic species previously documented by Matsuo and Eshima (1988); however, no taxonomic treatment of these populations was provided.

Recently, two studies have assessed the phylogenetic position of *Gekko* sp. from the Koshiki Islands populations within the subgenus *Japonigekko*. Cao et al. (2026) based on multilocus phylogenetic analysis of 324 conserved nuclear genes (nuDNA) and two fragments of mitochondrial genes (mtDNA) provided a well-resolved phylogeny for the subgenus *Japonigekko* and demonstrated that the two populations of *Gekko* sp. from the Koshiki Islands (referred to as *Gekko* sp. 2 in their paper) represent a distinct phylogenetic lineage forming a well-supported clade with *G. hokouensis* and *G. kaiyai* and are reconstructed as a sister species of the latter. Moreover, Okamoto et al. (2025) analyzed natural hybridization among seven species of *Gekko* using population genetic analysis based on microsatellite markers and allozyme data. They have demonstrated that *Gekko* sp. from the Koshiki Islands (referred to as *Gekko* sp. A in their study) is reproductively isolated from the sympatric *G. japonicus* and *G. hokouensis*, thus providing further evidence that it indeed might represent a new currently undescribed species.

In this study, we reassessed the taxonomic status of this cryptic *Gekko* lineage using an integrative approach that combines molecular phylogenetics and detailed morphological examinations. We conducted statistical comparisons of key morphological traits among the relevant species groups to evaluate diagnostic differences. In addition, we reconstructed a phylogenetic tree based on mitochondrial DNA sequences obtained from specimens, in order to clarify its evolutionary relationships with other congeners. Based on the combined evidence, we formally describe this cryptic lineage as a new species.

Material and methods

Sample collection

Field surveys were conducted from January 2024 to July 2025 (Fig. 1). After being photographed, all newly collected specimens were humanely euthanized using a lethal injection of 0.7% tricaine methanesulfonate (MS222) solution, then fixed in 95% ethanol one day and transferred to 75% ethanol for long-term preservation. Fresh liver tissue was extracted and immediately preserved in 95% ethanol and stored at –20 °C. The specimens were deposited at Museum of Natural and Environmental History, Shizuoka (**SPMN**): 5762 Oya, Suruga-ku, Shizuoka City, Shizuoka Prefecture 422-8017, Japan. All sampling procedures involving live geckos complied with the regulations of the Wildlife Protection Law of Japan.

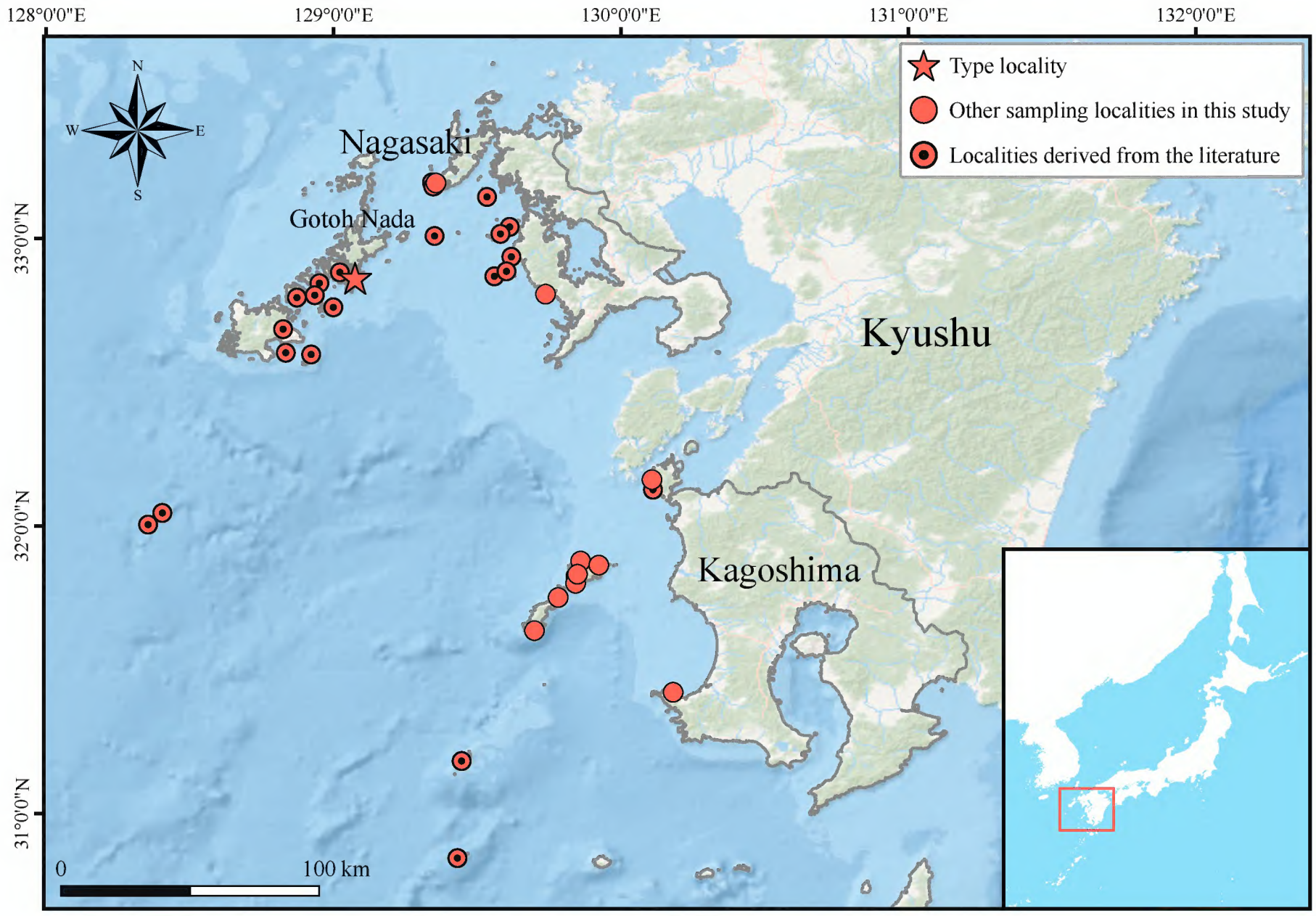

Figure 1. Map showing all known localities of *Gekko asahi* sp. nov. The star indicates the type locality, open circles represent sampling sites used in this study, and circles with a central dot indicate localities obtained from the literature. See Suppl. material 1: table S1 for detailed information.

Phylogenetic analyses

Genomic DNA was extracted from ethanol-preserved liver tissue using a standard phenol-chloroform-proteinase K (final concentration 1 mg/ml) extraction procedure with subsequent isopropanol precipitation (Hillis et al. 1996). DNA quality was assessed by agarose gel electrophoresis with ethidium bromide staining, and concentration was measured using a NanoDrop 2000 spectrophotometer (Thermo Scientific). DNA concentrations were adjusted to approximately 100 ng/µl. Two mitochondrial gene fragments, NADH dehydrogenase subunit 2 (*ND2*) and 16S ribosomal RNA (*16S*) were amplified via polymerase chain reaction (PCR) following the protocols outlined in Wang et al. (2024). The following primer pairs were used: rMet-3L (5'- ATACCCCGACAATGTTGG-3') and rAla-1H (5'- GCCTTAGCTTAATTAAAGTG-3') for *ND2* (Jonniaux and Kumazawa 2008); L3975 (5'-CGCCTGTTTACCAAAAACAT-3') and H4551 (5'-CCGGTCTGAACTCAGATCACGT-3') for *16S* (Simon et al. 1994). Positive PCR products were outsourced to Evrogen® (Moscow, Russia) for purification and sequencing. Raw sequences were assembled using SeqMan in the DNASTAR software package (Burland 2000). Newly generated sequences have been submitted to GenBank under accession numbers PZ033202–PZ033226 for *ND2*, and PZ014854–PZ014878 for *16S* (Table 1).

Apart from the 50 newly obtained sequences, we included 47 additional sequences representing 36 individuals from 34 species of the subgenus *Japonigekko*, which were retrieved from the public databases NCBI GenBank and DDBJ (Table 1). *Gekko gecko* (Linnaeus, 1758) and *G. reevesii* (Gray, 1831) were selected as outgroup, following the approach of Wang et al. (2024). A concatenated dataset of the two gene fragments (*ND2* 990 bp + *16S* 516 bp, 1,506 bp in total) was aligned using MUSCLE (Edgar 2004) in MEGA X (Kumar et al. 2018). The Maximum Likelihood (ML) analysis was conducted in IQ-TREE v1.6.12 (Nguyen et al. 2015) using the best-fit models GTR+F+I+R3 for the 16S fragment and TIM+F+R4 for the ND2 fragment, as determined by ModelFinder for IQ-Tree in PhyloSuite 1.2.3 according to Akaike information criterion (AIC) (Zhang et al. 2020; Kalyaanamoorthy et al. 2017; Akaike 1973, 1974). Node support was assessed using both the Ultrafast Bootstrap Approximation (UFB) and the SH-like approximate likelihood ratio test (SH). UFB values were calculated with 5,000 bootstrap replicates, with values ≥ 95% considered strong support; and SH was conducted with 1,000 replicates, and values ≥ 80% were regarded as well supported (Stephane et al. 2010; Hoang et al. 2018). Uncorrected pairwise distances (*p*-distances) between closely related species were also calculated in MEGA X (Kumar et al. 2018). The phylogenetic tree was visualized using FigTree v.1.4.4 (Rambaut 2018).

Table 1. NCBI/DDBJ accession numbers, localities, and voucher information for all specimens used in this study. * indicates DDBJ accession number.

No.	Species	Localities	Voucher ID	ND2	16S	References
1	*G. asahi* sp. nov	Nakadori, Nagasaki, Japan	TMR-66	PZ033202	PZ014854	**This study**
2	*G. asahi* sp. nov	Oitoku island, Hirado city, Nagasaki, Japan	SPMN-HP 003812 (TMR-85)	PZ033203	PZ014855	**This study**
3	*G. asahi* sp. nov	Okino island, Hirado city, Nagasaki, Japan	TMR-86	PZ033204	PZ014856	**This study**
4	*G. asahi* sp. nov	Okino island, Hirado city, Nagasaki, Japan	TMR-97	PZ033205	PZ014857	**This study**
5	*G. asahi* sp. nov	Okino island, Hirado city, Nagasaki, Japan	TMR-98	PZ033206	PZ014858	**This study**
6	*G. asahi* sp. nov	Okino island, Hirado city, Nagasaki, Japan	TMR-99	PZ033207	PZ014859	**This study**
7	*G. asahi* sp. nov	Miura peninsula, Nagasaki, Japan	SPMN-HP 003814 (TMR-117)	PZ033208	PZ014860	**This study**
8	*G. asahi* sp. nov	Minamisatsuma, Kagoshima, Japan	TMR-146	PZ033209	PZ014861	**This study**
9	*G. asahi* sp. nov	Minamisatsuma, Kagoshima, Japan	SPMN-HP 003815 (TMR-148)	PZ033210	PZ014862	**This study**
10	*G. asahi* sp. nov	Shimokoshiki Island, Kagoshima, Japan	TMR-159	PZ033211	PZ014863	**This study**
11	*G. asahi* sp. nov	Shimokoshiki Island, Kagoshima, Japan	TMR-160	PZ033212	PZ014864	**This study**
12	*G. asahi* sp. nov	Shimokoshiki Island, Kagoshima, Japan	SPMN-HP 003817 (TMR-161)	PZ033213	PZ014865	**This study**
13	*G. asahi* sp. nov	Shimokoshiki Island, Kagoshima, Japan	TMR-162	PZ033214	PZ014866	**This study**
14	*G. asahi* sp. nov	Nakakoshiki Island, Kagoshima, Japan	SPMN-HP 003818 (TMR-163)	PZ033215	PZ014867	**This study**
15	*G. asahi* sp. nov	Kamikoshiki Island, Kagoshima, Japan	TMR-166	PZ033216	PZ014868	**This study**
16	*G. asahi* sp. nov	Kamikoshiki Island, Kagoshima, Japan	SPMN-HP 003819 (TMR-167)	PZ033217	PZ014869	**This study**
17	*G. asahi* sp. nov	Kamikoshiki Island, Kagoshima, Japan	TMR-168	PZ033218	PZ014870	**This study**
18	*G. asahi* sp. nov	Kamikoshiki Island, Kagoshima, Japan	TMR-169	PZ033219	PZ014871	**This study**
19	*G. aaronbaueri*	Nakai District, Khammouan, Laos	NAP-09120	PZ033220	PZ014872	**This study**
20	*G. adleri*	Jingxi, Guangxi, China	SYS r001400	OR902178	MW451654	Lyu et al. 2021; Wang et al. 2024
21	*G. alpinus*	Mangkang, Xizang, China	CIB 121656	PQ303494	PQ255976	Ma et al. 2024
22	*G. auriverrucosus*	Anze County, Shanxi, China	SWU 0006819	PZ033221	PZ014873	**This study**
23	*G. bonkowskii*	Thakhek Town, Khammouane, Laos	VFU R.2014.10	KT266818	–	Luu et al. 2015
24	*G. cib*	Hejiang, Sichuan, China	SYS r001489	OR902165	MW451655	Lyu et al. 2021; Wang et al. 2024
25	*G. chinensis*	Hong Kong, China	SYS r001211	OR902183	MW451644	Lyu et al. 2021; Wang et al. 2024
26	*G. fengshanensis*	Fengshan, Hechi, Guangxi, China	NHMG 202408005	PV657379	PV652775	Huang et al. 2025
27	*G. hokouensis*	Mt. Wuyi, Fujian, China	SYS r001290	OR902173	MW451647	Lyu et al. 2021; Wang et al. 2024
28	*G. hokouensis*	Mt. Meiling, Jiangxi, China	SYS r001311	OR902172	MW451648	Lyu et al. 2021; Wang et al. 2024
29	*G. ichangensis*	Changyang County, Hubei, China	SWU 0011608	PZ033222	PQ587509	**This study**; Cao et al. 2025
30	*G. japonicus*	Lushan, Jiangxi, China	SYS r001317	OR902177	MW451649	Lyu et al. 2021; Wang et al. 2024
31	*G. jinjiangensis*	Deqin, Yunan, China	CIB 5334220088	MT449432	PQ255987	Hou et al. 2021; Ma et al. 2024
32	*G. kaiyai*	Xin County, Henan, China	SWU 0010510	PZ0332203	PZ014875	**This study**
33	*G. kaiyai*	Xinxian, Xinyang, Henan, China	AHUXXBH01	–	OQ780318	Zhang et al. 2023
34	*G. khunkhamensis*	Khunkham District, Khammouane, Laos	VNUF R.2021.23	OL416111	–	Sitthivong et al. 2021
35	*G. kwangsiensis*	Wuming, Guangxi, China	SYS r001195	OR902175	MW451642	Lyu et al. 2021; Wang et al. 2024
36	*G. liboensis*	Maolan, Libo, Guizhou, China	SYS r002876	PV657381	PV652777	Huang et al. 2025
37	*G. melli*	Dongguan, Guangdong, China	SYS r001742	OR902169	MW451661	Lyu et al. 2021; Wang et al. 2024
38	*G. nadenensis*	Khammouane, Laos	ZFMK 98741	KY421618	–	Luu et al. 2017
39	*G. palmatus*	Mt.Dinghu, Guangdong, China	SYS r002797	OR902179	OR903156	Wang et al. 2024
40	*G. paucituberculatus*	Baise, Guangxi, China	SYS r002806	OR902163	OR903154	Wang et al. 2024
41	*G. prep*	Changjiang, Hainan, China	HN2024R038	PV389916	PV368865	Zhou et al. 2025a
42	*G. scabridus*	Yanbian, Sichuan, China	CIB YN201909199	MT449429	PQ255992	Hou et al. 2021; Ma et al. 2024
43	*G. scientiadventura*	Minh Hoa District, Quang Binh, Vietnam	NAP-13792	PZ033224	PZ014876	**This study**
44	*G. sengchanthavongi*	Bualapha Town, Khammouane, Laos	VFU R.2014.14	KT266816	–	Luu et al. 2015
45	*G. similignum*	Wuzhishan, Hainan, China	SYS r001597	OR902185	MW451658	Lyu et al. 2021; Wang et al. 2024

No.	Species	Localities	Voucher ID	ND2	16S	References
46	*G. subpalmatus*	Fenghua, Zhejiang, China	SYS r001762	OR902167	MW451662	Lyu et al. 2021; Wang et al. 2024
47	*G. swinhonis*	Zunhua, Hebei, China	SYS r001814	OR902171	MW451666	Lyu et al. 2021; Wang et al. 2024
48	*G. tawaensis*	Saiki City, Oita, Japan	TMR83	PZ033225	PZ014877	**This study**
49	*G. tesselatus*	Heishui, Sichuan, China	CIB 119371	LC899318*	LC899308*	Xu et al. 2025
50	*G. thakhekensis*	Thakhek, Khammouane, Laos	IEBR A.2014.6	KP205396	–	Luu et al. 2014
51	*G. truongi*	Ninh Hoa District, Khanh Hoa, Vietnam	IEBR A.2011.1	KP205398	–	Luu et al. 2014
52	*G. wenxianensis*	Wenxian County, Gansu, China	SWU 0010311	PZ033226	PZ014878	**This study**
Out group						
53	*G. gecko*	Nanning, Guangxi, China	N/A	AY282753	AY282753	Zhou et al. 2006
54	*G. reevesii*	Mt. Yinping, Guangdong, China	SYS r000796	OR902187	MW451630	Lyu et al. 2021; Wang et al. 2024

Morphological analyses.

Measurements were taken with digital calipers (Shinwa digital caliper) to the nearest 0.1 mm on the right side of the body, and scalation features were counted under a binocular scope (ST-30-2L, AS ONE CORPORATION). Bilateral scale counts are given as left/right. External measurements, meristic traits and their abbreviations followed Wang et al. (2024) and Huang et al. (2025). External measurements are snout-vent length (**SVL**, from tip of snout to anterior margin of cloaca); axillia groin length (**AG**, distance between axilla and groin); head length (**HL**, from tip of snout to posterior margin of ear opening); head width (**HW**, at the angle of the jaws); head height (**HH**, from the top of the head posterior to the eyes to the bottom of the lower jaw); internarial distance (**IND**, across the snout between the dorsal margins of the external nares); orbital diameter (**OD**, the horizontal diameter of the bony orbit); eye to ear distance (**EE**, from the anterior margin of the auricular opening to the posterior margin of the eyeball); eye length (**EL**, eye diameter, measured as the greatest distance from the anterior to the posterior corner of the eye); snout-eye length (**SE**, from anterior most margin of the eyeball to the tip of snout); nares-eye length (**NE**, from the anterior margin of the eyeball to the posterior margin of the external nares); forelimb length (**FLL**, from the distal edge of the elbow when flexed 90° to the wrist); and hindlimb length (**HLL**, from the distal edge of the knee when flexed 90° to the ankle); cloaca length (**CL**, at the cloaca of base of tail).

Meristic characters are as follows: supralabials and infralabials (**SPL** and **IFL**, number of scales from commissure of jaw to the rostral /mental scale); internasal scales (**IS**, number of scales in the nasal space); preorbitals (**PO**, number of scales in a line from the nostril to the anterior margin of the eye); postmentals (**PM**, number of scales bordering the mental); interorbitals (**IOS**, number of scales in a line between anterior margins of eyes); scales in a line from mental to the front of cloacal slit (**SMC**); number of scale rows around midbody (**SR**, including ventral scales); ventral scale rows at midbody between ventrolateral folds (**VS**); paravertebral tubercles (**PVT**, number of longitudinally arranged tubercles between an imaginary line between the middle of the limb insertions); longitudinal rows of tubercles (**LRT**, the dorsum between the ventrolateral body folds midway between the limb insertions); sub-digital lamellae under entire first finger (**LF1**); sub-digital lamellae under entire fourth finger (**LF4**) sub-digital lamellae of entire first toe (**LT1**); sub-digital lamellae of entire fourth toe (**LT4**); precloacal pores (**PP**); and postcloacal tubercles (**PAT**). In addition, we also recorded the presence or absence of webbing (**Web**); the presence of tubercles on the forelimbs (**Fore tubercles**), hindlimbs (**Hind tubercles**), tail (**Tail tubercles**); number of rounded patterns on dorsum (**Dorsal rounded patterns**); number of crossbands on tail (**Tail crossbands**); the presence of enlarged subcaudal scales; and the types of dorsal coloration patterns.

Morphological data of other subgenus *Japonigekko* species were taken from the literature (e.g., Stejneger 1907; Zhou et al. 1982; Song 1985; Ota et al. 1995; Zhao et al. 1999; Rösler et al. 2005; Toda et al. 2008; Zhou and Wang 2008; Rösler et al. 2011; Phung and Ziegler 2011; Nguyen et al. 2013; Luu et al. 2014, 2015, 2017; Ngo et al. 2015; Yang 2015; Lin and Yao 2016; Hou et al. 2021; Lyu et al. 2021; Sitthivong et al. 2021; Zhang et al. 2023; Ma et al. 2024; Song et al. 2024; Wang et al. 2024; Cao et al. 2025; Huang et al. 2025; Xu et al. 2025; Zhou et al. 2025a, 2025b).

Statistical analysis

Among the examined populations, SVL was compared using a one-way ANOVA with the Tukey-Kramer test. The percentage ratio (R) of each morphometric character to SVL was subsequently calculated; we compared character ratios against SVL among populations using the Kruskal-Wallis test. To further assess morphological differentiation among *Gekko* sp. from the Koshiki Islands and its closest relatives (*G. hokouensis* and *G. kaiyai*; data for the latter two species were obtained from Zhang et al. 2023, see below), we conducted a Principal Component Analysis (PCA) in order to examine overall morphological variation among populations using log-transformed metric values following Nishikawa et al. (2007). When a high correlation between certain pairs of characters was found, we omitted one of them from the analyses to exclude possible overweighting effects; overall, the SVL and 13 character ratios (AG/SVL, HW/SVL, HL/SVL,

HH/SVL, SE/SVL, NE/SVL, EE/SVL, EL/SVL, IND/SVL, OD/SVL, FLL/SVL, HLL/SVL, and CL/SVL) were included in the PCA analysis. Statistical analyses were performed with Statistica 6.0 (StatSoft Inc. 2001). The significance level was $P < 0.05$.

Results

Phylogenetic analysis

The ML analyses resulted in the topology shown in Fig. 2. Mean uncorrected *p*-distances based on the *ND2* and *16S* genes are summarized in Suppl. material 1: tables S2, S3, respectively. All *Gekko* (*Japonigekko*) samples used in this study formed a strongly supported monophyletic lineage (SH = 100 / UFB = 100). However, relationships among species within the subgenus remain only partially resolved due to low nodal support at several interspecific nodes. Eighteen samples from Nagasaki and Kagoshima Prefectures, Kyushu District, Japan were recovered as a well-supported independent lineage (SH = 100 / UFB = 100) within the subgenus *Japonigekko*. This lineage showed very low internal genetic divergence, ranging from 0.0% to 2.5% in *ND2* and from 0.0% to 0.6% in *16S*. It was inferred to be the sister lineage of *G. kaiyai* Zhang, Wu & Zhang, 2023, although the support for this relationship was low (SH = 60 / UFB = 78). These two lineages together formed a strongly supported clade with *G. hokouensis* (SH = 100 / UFB = 100) (which we refer to as the *G. hokouensis* clade below).

The uncorrected *p*-distances between the unnamed lineage and other members of *Japonigekko* ranged from 15.1% (vs. *G. kaiyai*) to 26.2% (vs. *G. adleri* Nguyen, Wang, Yang, Lehmann, Le, Ziegler & Bonkowski, 2013) in *ND2* (Suppl. material 1: table S2), and 7.6% (vs. *G. hokouensis*) to 16.4% (vs. *G. adleri*) in *16S* (Suppl. material 1: table S3). These values are markedly greater than the smallest interspecific

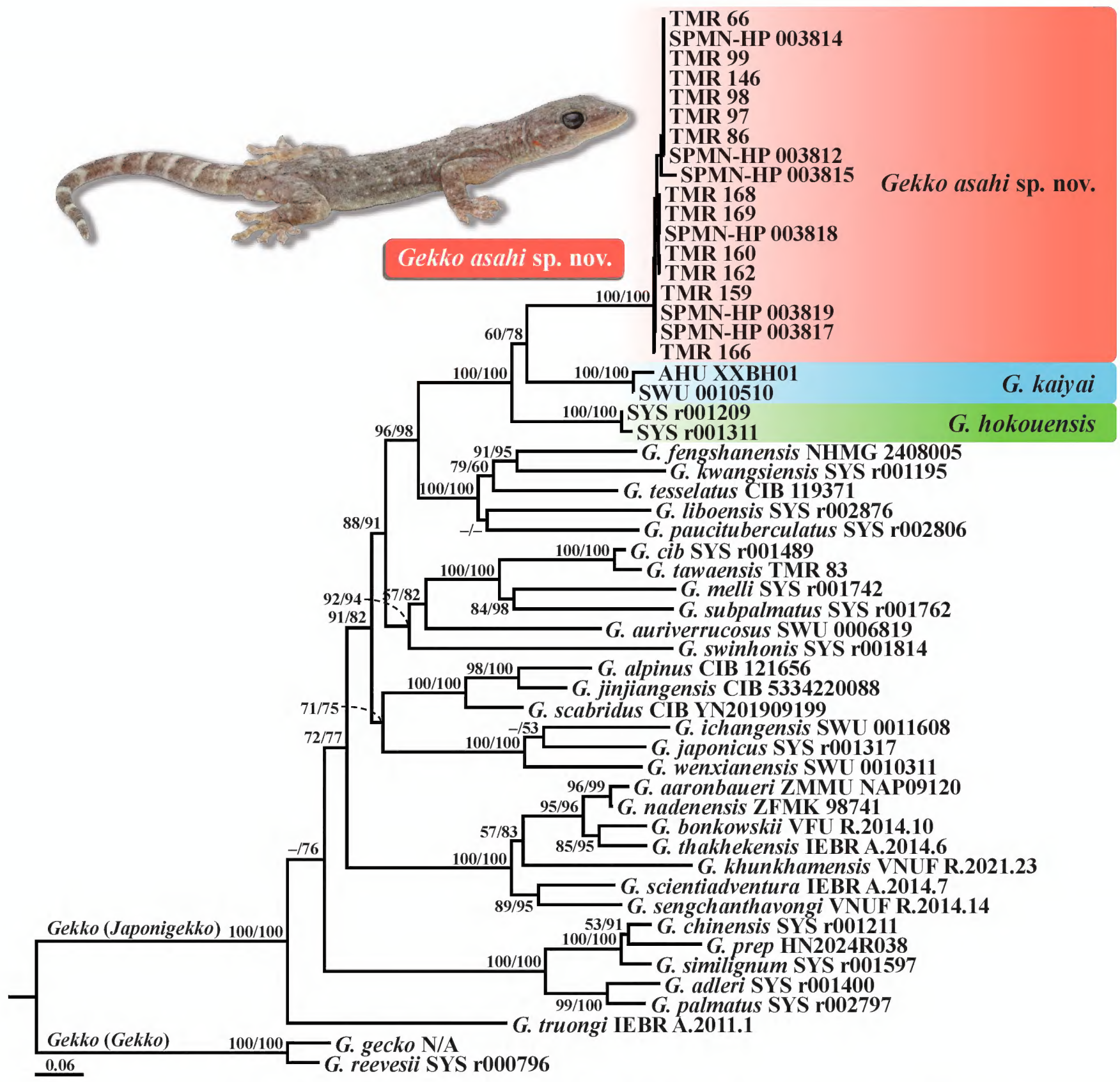

Figure 2. Maximum likelihood (ML) tree of *Japonigekko* inferred from *ND2* and *16S* genes. Node support values are presented as SH-like approximate likelihood ratio test (SH) / ultrafast bootstrap approximation (UFB); those lower than 50 are shown as "–". Photograph on thumbnail by T. Matsukoji.

divergences recovered within the subgenus in this study, namely 3.3% between *G. cib* Lyu, Lin, Ren, Jiang, Zhang, Qi & Wang, 2021 and *G. tawaensis* in *ND2*, and 2.2% between *G. chinensis* and *G. similignum* Smith, 1923 in *16S* (Suppl. material 1: tables S2, S3). This indicates that the population from Nagasaki and Kagoshima Prefectures is genetically distinct from all recognized congeners.

Morphological analysis

All examined characters exhibit normal distributions in all datasets. The univariate analysis revealed statistically significant differences between the three molecular Operational Taxonomic Units (mOTUs) of the *G. hokouensis* clade in body ratios (divided by SVL). The P-values associated with the univariate morphological comparisons among the three members of the *G. hokouensis* clade are summarized in Suppl. material 1: table S4. Univariate analyses for both the male, female, and combined datasets showed significant differentiation in the SVL, AG/SVL, HW/SVL, HL/SVL, HH/SVL, SE/SVL, EE/SVL, EL/SVL, IND/SVL, and FLL/SVL between the three mOTUs (Suppl. material 1: table S4).

PCA plots revealed that all three mOTUs show no overlap in the morphospace (Fig. 3). PCA1 accounted for 30.36% of the total variance and loaded most heavily on SE/SVL, NE/SVL, and EE/SVL. PCA2 accounted for 16.20% of the total variance and loaded most heavily on EL/SVL, HH/SVL, HL/SVL, and HLL/SVL. More details on the PCA results can be found in Suppl. material 1: table S5. Overall, the morphometric data was distributed in three non-overlapping clusters corresponding to each member of the *G. hokouensis* clade, with *G. kaiyai* occupying a more distant position from the two remaining species in the morphospace (Fig. 3).

Furthermore, morphologically, the newly collected specimens also show clear and diagnosable differences from all known species of the subgenus *Japonigekko* in a number of scalation and coloration characters which are summarized below in the Comparisons section. Therefore, given the unambiguous differences of the unnamed population of *Gekko* sp. from Nagasaki and Kagoshima Prefectures, Kyushu District, Japan, both in molecular and morphological characters, we formally describe it below as a new species.

Taxonomic account

Family Gekkonidae Oppel, 1811
Genus *Gekko* Laurenti, 1768
Subgenus *Japonigekko* Wood, Guo, Travers, Su, Olson, Bauer, Grismer, Siler, Moyle, Andersen & Brown, 2020

***Gekko asahi* Matsukoji, Cao, Poyarkov, Okamiya, Xu & Yuan, sp. nov.**

https://zoobank.org/B3B4F3BF-453B-4B33-B25A-0526314C5083

Figs 4–7, Table 2, Suppl. material 1: table S6.

Chersonymy:

Gekko sp. — Morita (1987); Morita (1988); Matsuo et al. (1988); Matsuo and Ejima (1988); Tokunaga (1988); Matsuo and Ejima (1989a); Matsuo and Ejima (1989b); Sengoku (1989); Shibata (1990); Matsuo (2019).

Gekko sp. 1 — Okamoto and Toda (2022).

Gekko sp. 2 — Cao et al. (2026).

Gekko sp. A — Jono (2016); Okamoto et al. (2025).

Holotype. • SPMN-HP 003810 (Field NO. TMR-65, adult male) from Nakadori Island, Shinkamigoto Town, Nagasaki Prefecture, Kyushu District, Japan (32.8611°N, 129.0756°E; 3 m asl.), collected by Seiji Tsujita on January 08, 2024.

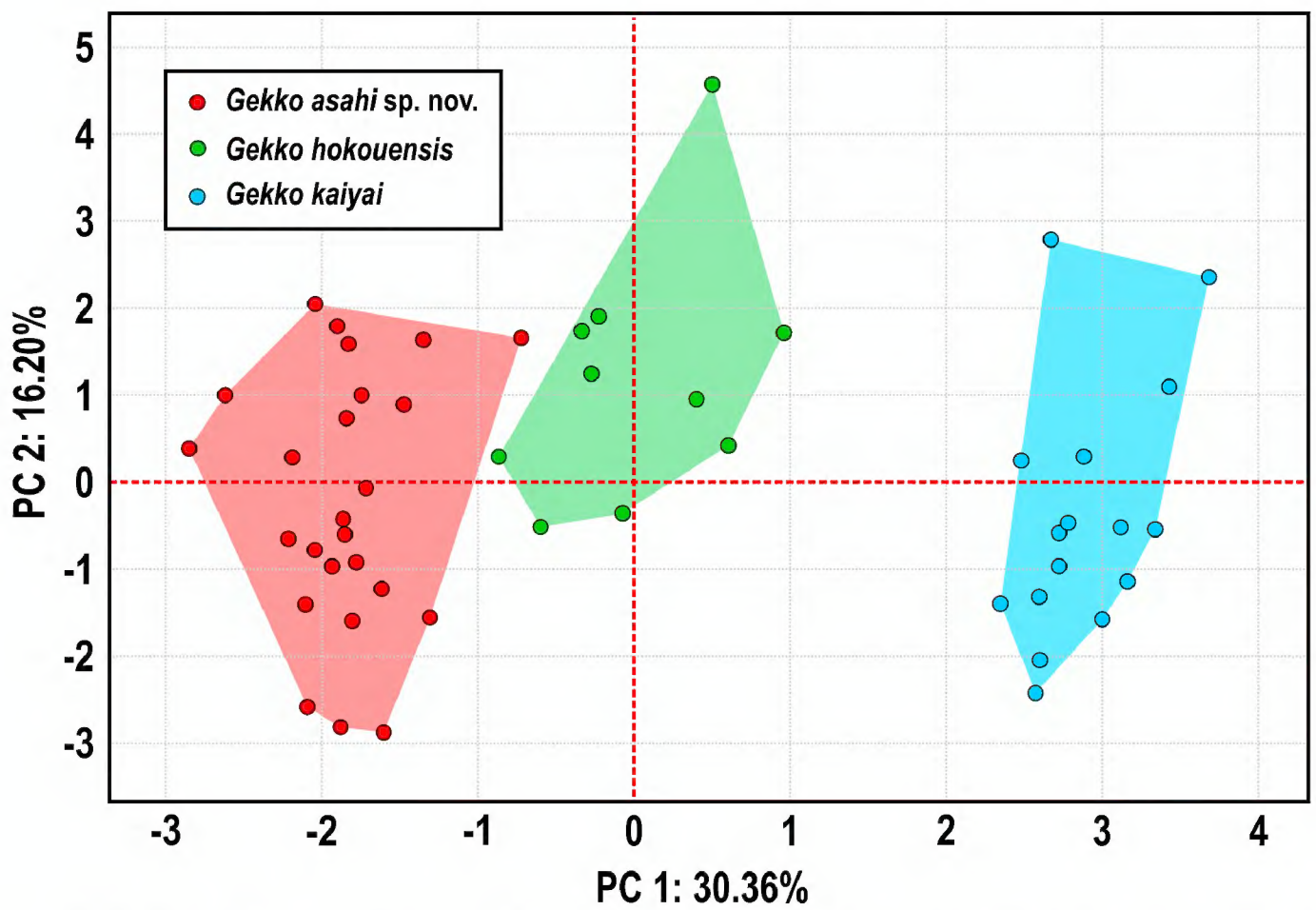

Figure 3. PCA scatter plots of *Gekko asahi* sp. nov., *G. hokouensis*, and *G. kaiyai*. The PCA results for the dataset combining male and female are shown. The shape and color indicated signify different clusters of each *Gekko* spp.

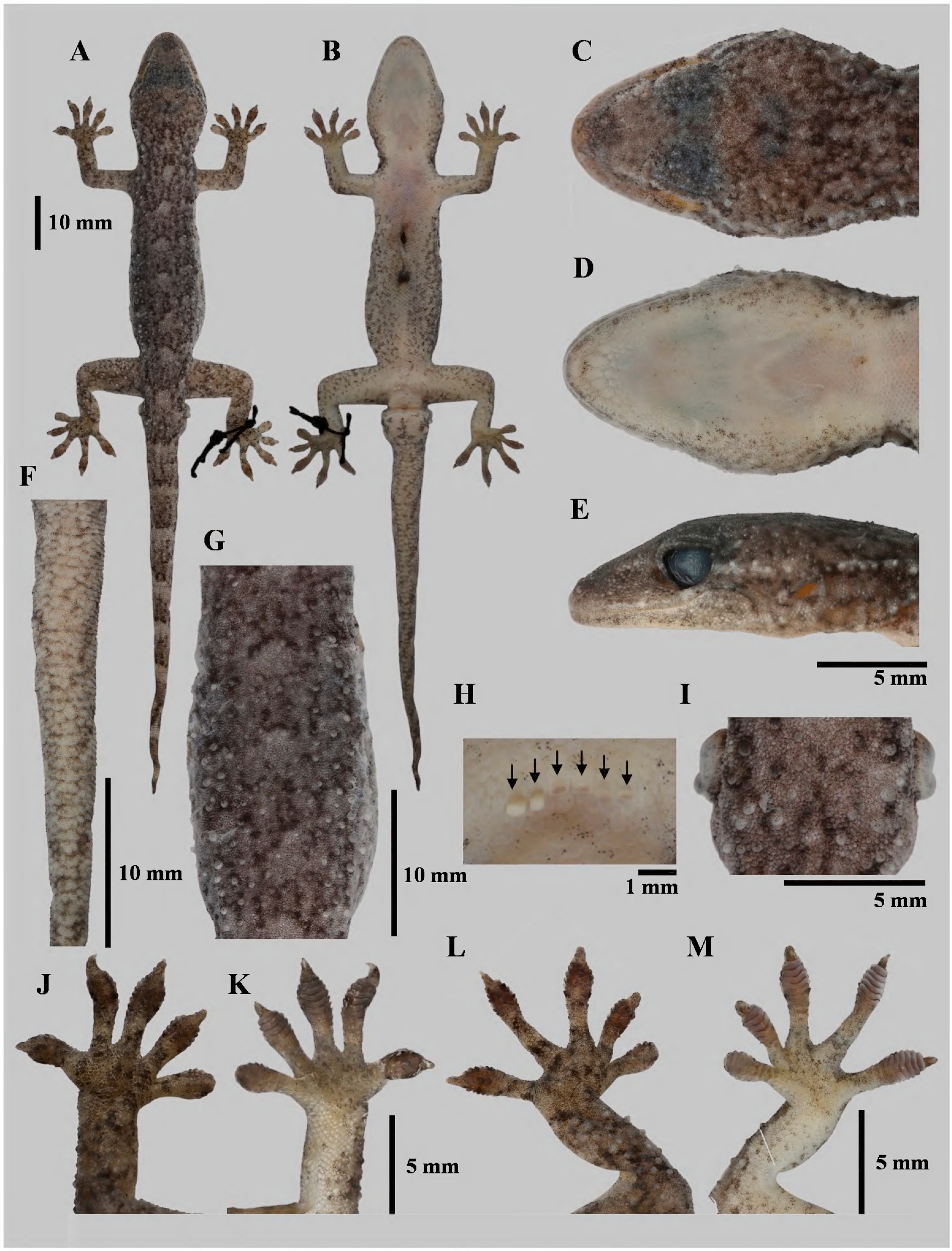

Figure 4. Preserved specimen of the holotype of *Gekko asahi* sp. nov. (SPMN-HP 003810, male). **A.** Dorsal view; **B.** Ventral view; **C.** Dorsal view of head; **D.** Ventral view of head; **E.** Left side of head; **F.** Ventral view of tail; **G.** Dorsal view of midbody; **H.** Precloacal pores; **I.** Postcloacal tubercles; **J.** Dorsal view of fore limb; **K.** Ventral view of fore limb; **L.** Dorsal view of hind limb; **M.** Ventral view of hind limb. Photographs by T. Matsukoji.

Paratypes (N = 9, Nagasaki and Kagoshima Prefectures, Japan). • SPMN-HP 003811 (Field NO. TMR-69, adult female) from the same locality of the holotype, collected by Seiji Tsujita; • SPMN-HP 003812 (Field NO. TMR-85, adult male) from Okinoshima Island, Noko Town, Hirado City, Nagasaki Prefecture (33.1921°N, 129.3567°E; 2.5 m asl.) collected by Tomoya Matsukoji on September 23, 2024; • SPMN-HP 003813 (Field NO. TMR-104, adult male) from Hirado Island, Noko Town, Hirado City, Nagasaki Prefecture (33.1815°N, 129.3502°E; 3 m asl.), collected by Tomoya Matsukoji on September 23, 2024; • SPMN-HP 003814 (Field NO. TMR-117, adult male) from Kashiyama Town, Nagasaki City, Nagasaki Prefecture (32.8061°N, 129.7375°E; 2.5 m asl.), collected by Tomoya Matsukoji, Masahiro Nagano, Yusuke Fuji on November 04, 2024; • SPMN-HP 003815 (Field NO. TMR-148, adult female) from Kasasa Town, Minamisatsuma City, Kagoshima Prefecture (31.4213°N, 130.1815°E; 2 m asl.), collected by Tomoya Matsukoji on July 07, 2025; • SPMN-HP 003816 (Field NO. TMR-149, adult male) from Nagashima Island, Nagashima Town, Kagoshima Prefecture (32.1609°N, 130.1082°E; 5 m asl.), collected by Tomoya Matsukoji on July 07, 2025; • SPMN-HP 003817 (Field NO. TMR-161, adult female) from Shimo-Koshiki Island, Satsumasendai City, Kagoshima Prefecture (31.6361°N, 129.6996°E; 5 m asl.), collected by Tomoya Matsukoji on July 05, 2025; • SPMN-HP 003818 (Field NO. TMR-163, adult female) from Naka-Koshiki Island, Satsumasendai City, Kagoshima Prefecture (31.8005°N, 129.8424°E; 2 m asl.), collected by Tomoya Matsukoji on July 05, 2025; • SPMN-HP 003819 (Field NO. TMR-167, adult female) from Kami-Koshiki Island, Satsumasendai City, Kagoshima Prefecture (31.8778°N, 129.8599°E; 50 m asl.), collected by Tomoya Matsukoji on July 05, 2025.

Additional specimens (N = 15): • TMR-62 (adult male), • TMR-70 (adult female) from the same locality and date of the holotype, collected by Seiji Tsujita; • TMR-86, • TMR-88 (adult male), • TMR-96 and • TMR-97 (adult female) from the same locality and date of the paratype SPMN-HP 003812; • TMR-106 (adult female) from the same locality and date of the paratype SPMN-HP 003813, • TMR-119 (adult female) from the same locality and date of the paratype SPMN-HP 003814; • TMR-169, • TMR-197 (adult female) and • TMR-190 (adult male) from the same locality and date of the paratype SPMN-HP 003819; • TMR-170 (adult female), • TMR-173 and • TMR-196 (adult male) from the same locality and date of the paratype SPMN-HP 003817; • TMR-183 (adult male) from the same locality and date of the paratype SPMN-HP 003818.

Etymology. The specific epithet "*asahi*" is treated as an indeclinable noun in apposition. It is derived from the Japanese word "朝日" (あさひ, *asahi*), meaning "morning sun" or "rising sun". The name refers to the slightly faint yellow to light orange-red coloration present on the body and limbs, as well as the bright reddish yellow to pale golden-yellow coloration of the ventral surface of the new species, which resembles the warm hue of the early morning sunlight. For the common names, we suggest "West Japanese Gecko" in English, "ニシヤモリ"(*Nishi-yamori*) in Japanese, "晨曦壁虎" (*chén xī bì hǔ*) in Chinese, and "Западнояпонский геккон" (*Zapadnoyaponskiy gekkon*) in Russian.

Diagnosis. *Gekko asahi* sp. nov. can be diagnosed from other *Japonigekko* species by the following unique combination of characters: (1) a moderate body size (SVL reaches up to 73.85 mm in males and 73.96 mm in females); (2) 6–9 supralabials and 6–8 infralabials; (3) internasal scales absent; (4) two postmentals; (5) 14–18 preorbitals; (6) 34–44 interorbital scales; (7) 158–189 ventral scales between the mental and the cloacal slit; (8) 127–158 midbody scale rows; (9) 32–45 ventral scale rows; (10) prominent dorsal tubercles present from the posterior head through the neck to the anterior portion of the tail, arranged in 12–16 rows at midbody and numbering 17–23 tubercles along a longitudinal line on the dorsum between the limb insertions; (11) subdigital lamellae 8–11 on finger I, 9–14 on finger IV, 9–12 on toe I, and 10–18 on toe IV; (12) webbing absent; (13) 6–9 precloacal pores in males, absent in females; (14) one postcloacal tubercle on each side, with the midpoint of the tubercle distinctly concave in some male individuals; (15) in life, the dorsum is predominantly yellowish-gray, with 8–9 indistinct pale yellowish-brown rounded patterns, and venter is pale golden-yellow in color.

Description of the holotype (Fig. 4, Suppl. material 1: table S6). An adult male with original tail. Size medium, SVL 60.69 mm; body slender and trunk relatively elongate, AG 25.49 mm, AG/SVL ratio 0.42.

Head depressed, noticeably longer than wide, and clearly separated from the neck, HL 15.18 mm, HW 12.24 mm, HH 6.6 mm, HL/SVL ratio 0.25, HW/SVL ratio 0.2, HW/HL ratio 0.81, HH/HL ratio 0.43. Snout obtuse, round anteriorly, SE 7.03 mm, SE/HL ratio 0.46. Relatively longer, NE 5.45 mm, NE/HL ratio 0.4. EE 5.71 mm, EE/HL ratio 0.38. EL 2.9 mm, EL/HL ratio 0.19; pupil vertical, featuring crenulated edges. IND 2.1 mm, IND/HL ratio 0.14. OD 5.07 mm, OD/HL ratio 0.33.

Rostral approximately rectangular in shape, wider than the high. Nares oval, rounded by the rostral, 1st supralabial, one distinctly enlarged supranasal and three slightly enlarged nasals posteriorly; internasals absent. Preorbitals 15, preorbital region deeply concave; interorbital scales between the anterior corners of eyes 37; supralabials 7/7; infralabials 6/6. Mental pentagonal, wider than long, and slightly narrower than the rostral; postmentals two, enlarged, twice as long as wide, touching the mental and the first infralabial on both sides and three gular scales posteriorly. Tubercles are enlarged and strongly elevated, present on the lateral surfaces of the head behind the eyes.

Table 2. Morphological characters of *Gekko* (*Japonigekko*), bold fonts indicate the difference with the new species; Y = "Yes" or present, N = "No" or absent.

No.	Species	SVLmax	SPL	IFL	IO	DTR	SMC	SR	V	LT1	LT4	Web	Fore tubercles	Hind tubercles	Tail tubercles	PP
1	*G. asahi* sp. nov.	73.96	7–9	6–9	34–44	12–16	158–193	127–158	32–45	9–12	10–18	N	Y	Y	Y	6–9
2	*G. aaronbaueri*	80	**13–14**	**10–11**	34–37	**0**	–	**98–104**	39–43	**14–17**	14–16	**Y**	**N**	**N**	**N**	**3–4**
3	*G. adleri*	75.3	**10–15**	9–13	27–36	**7–11**	168–190	123–144	35–44	11–14	11–15	**Y**	**N**	Y	Y	**17–21**
4	*G. alpinus*	74.16	9–13	8–10	**22–28**	12–17	158–189	**92–114**	32–39	8–11	13–15	N	Y	Y	Y	4–7
5	*G. auriverrucosus*	69	9–11	9–11	**26–27**	16–20	–	–	–	**6–8**	**6–8**	N	Y	Y	Y	8–11
6	*G. bonkowskii*	69.2	**12–14**	**10–11**	**49–50**	**0**	154–169	**117**	37–40	11–13	15	**Y**	**N**	**N**	**N**	6
7	*G. canhi*	99.2	**14**	**10–12**	**49–50**	11–12	168–170	**205–227**	**49–51**	**13–16**	14–17	N	**N**	Y	**N**	5
8	*G. chinensis*	72	**10–14**	9–13	35–48	**10**	156–167	118–140	37–39	8–10	9–12	**Y**	**N**	Y	Y	**17–2**7
9	*G. cib*	66.4	**10–12**	**10–14**	28–36	**0**	171–196	128–149	37–45	9–13	9–17	**Y**	**N**	**N**	**N**	7–9
10	*G. fengshanensis*	79.9	9–13	**10–13**	**22–27**	**9–11**	**197–213**	149–161	40–49	12–14	13–15	**Y**	**N**	**N**	**N**	9–12
11	*G. guishanicus*	64	–	–	–	**0**	–	–	–	8–10	8–10	**Y**	**N**	**N**	**N**	6–8
12	*G. hokouensis*	70	**10–14**	8–11	**30–33**	12–18	153–174	119–130	36–43	8–11	15–18	N	**N**	**N**	Y	5–9
13	*G. ichangensis*	66.5	7–11	7–11	27–36	10–12	174–195	127–145	39–47	12–15	13–18	**Y**	Y	Y	Y	5–8
14	*G. japonicus*	74	9–13	8–13	32–35	9–14	169–188	130–144	39–44	10–12	14–16	N	Y	Y	Y	4–9
15	*G. jinjiangensis*	61.6	7–10	6–9	**20–24**	12–16	146–169	111–149	31–47	**8–11**	11–15	N	Y	Y	Y	**4–5**
16	*G. kaiyai*	64.99	9–12	9–13	**22–33**	11–18	157–209	**99–121**	30–43	8–9	7–11	N	Y	Y	Y	9–12
17	*G. khunkhamensis*	75.2	9–10	9–10	**31–32**	**0**	181–185	127–138	42–45	**13–14**	14–15	**Y**	**N**	**N**	**N**	**0**
18	*G. kwangsiensis*	69.7	**10–12**	**11–13**	**29–31**	**9–11**	185–208	143–156	41–45	11–13	13–18	**Y**	**N**	**N**	Y	9–11
19	*G. liboensis*	79.7	**11**	9–11	32–35	**9–10**	183–195	131–140	38–41	12–13	14–15	**Y**	**N**	**N**	–	9
20	*G. liui*	56.67	**11–13**	**11–12**	37–42	**7–8**	**140–148**	**103–118**	34–39	10–11	12–13	**Y**	**N**	**N**	Y	**20–23**
21	*G. melli*	80.3	**10–13**	9–12	34–40	**0**	171–192	148–160	44–46	10–12	11–14	**Y**	**N**	**N**	**N**	9–11
22	*G. nadenensis*	77.1	**12–14**	**10–12**	**28–30**	**0**	175–185	123–140	38–40	**13–15**	14–16	**Y**	**N**	**N**	**N**	6
23	*G. palmatus*	79.7	**11–15**	9–13	27–36	4–12	160–191	116–147	36–47	10–13	10–16	**Y**	**N**	**N**	Y	**23–30**
24	*G. paucituberculatus*	85.9	**11**	9–10	37	**4**	189–192	136–140	42–44	11	11–13	**Y**	**N**	**N**	**N**	**12**
25	*G. prep*	75.7	**14**	**11**	37–38	12	**144–152**	**122–126**	38–40	11–12	12–13	**Y**	**N**	**N**	Y	**24**
26	*G. scabridus*	64	9–11	9–11	**30**	**17–21**	–	–	–	6–9	**7–9**	N	Y	Y	Y	10–15
27	*G. scientiadventura*	73	**12–1**4	9–13	41–51	**0**	**118–140**	139–143	38–48	12–15	14–17	**Y**	**N**	**N**	Y	**23–30**
28	*G. sengchanthavongi*	77.3	8–10	6–7	**28–32**	**0**	175–184	120–135	35–43	11–14	13–17	**Y**	**N**	**N**	**N**	**4–5**
29	*G. shibatai*	70.9	**10–13**	**10–14**	37–52	5–14	–	114–134	–	11–12	9–16	N	**N**	**N**	Y	**0–3**
30	*G. similignum*	58.9	**12–14**	**11**	**46–48**	**11**	–	144–153	–	11–13	12–14	**Y**	**N**	**N**	Y	**17**
31	*G. subpalmatus*	65.8	8–12	7–12	28–37	**0**	144–190	129–156	39–46	9–12	11–14	**Y**	**N**	**N**	**N**	5–9
32	*G. swinhonis*	66	7–12	7–11	**23–24**	**6–**8	–	–	40	6–9	**6–9**	N	Y	Y	–	7–9
33	*G. taibaiensis*	69	9–10	8–10	**28**	**–**	–	–	–	**6–7**	**7–8**	**Y**	–	–	–	4–6
34	*G. tawaensis*	71	9–10	8–10	**28**	**0**	184–190	131–152	40–43	10	12	N	**N**	**N**	**N**	**0**
35	*G. tesselatus*	65.3	**10 or 11**	9–12	**22–26**	12–15	**130–157**	**98–106**	31–39	7–9	9–12	N	**N**	Y	Y	6–8
36	*G. thakhekensis*	79.2	**12–14**	**10–11**	**22–26**	**0**	165–174	**110–116**	32–40	11–13	14–15	**Y**	**N**	**N**	**N**	**1–5**
37	*G. truongi*	95.9	**13–15**	**11–13**	**45–48**	**0**	160–172	131–143	35–36	11–13	15–17	N	**N**	**N**	**N**	10–11
38	*G. vertebralis*	69.2	**10–15**	**10–15**	35–50	2–12	–	112–139	**10–12**	–	9–17	N	**N**	**N**	**N**	**0–1**
39	*G. wenxianensis*	59	**12**	**11**	–	**10**	–	–	42–44	**6**	**9**	N	**N**	Y	–	6–8
40	*G. yakuensis*	72	**12–13**	9–13	–	–	–	–	–	10	15	N	**N**	**N**	Y	6–8

Dorsal scales smooth, round to oval, granular, and juxtaposed. Tubercles distinctly raised, irregularly arranged, extending from the posterior part of the head to the anterior one-third of the tail, forming approximately 13 rows at midbody, and with 19 tubercles along a longitudinal line on the dorsum between the limb insertions. Ventrolateral fold present, without tubercles; ventrals slightly larger than dorsals, smooth, imbricate, and largest in middle of belly; ventral scale rows at midbody 38; scale rows around midbody 137; ventral scales in a row between mental and cloacal slit 174; precloacal scales enlarged, but no enlarged scales on thighs; precloacal pores six (Figs 4H, 5A); postcloacal tubercles 1/1, large, with the midpoint of each tubercle distinctly concave. Dorsal scales of tail flat and smooth, irregular in size, with a few tubercles present on the anterior one-third of the tail; subcaudals small at the base, distinctly enlarged beyond the swollen portion, and arranged in a longitudinal row.

Forelimbs and hindlimbs well-developed; dorsal surface of the upper forelimb lacks tubercles, whereas the lower forelimb bears tubercles; the hindlimbs have tubercles across the entire dorsal surface. No webbing between the fingers and toes; digits moderately dilated; fingers and toes II–IV clawed; claws laterally compressed, extending beyond the terminal lamellae; no webbing between fingers and toes; subdigital lamellae undivided, 8 on finger I (left), 9 on finger IV (left), 10 on toe I (left), and 15 on toe IV (ledt); relative length of fingers and toes I < II < V < III < IV.

Coloration of the holotype in life. In life, the ground color on the dorsal surface of the head was yellowish gray, extending from the snout and eyelids to the posterior margin of the head. The dorsal ground color of the body was grayish brown, bearing eight indistinct, pale yellowish-brown rounded blotches from the neck to the base of the tail. These blotches were aligned along the vertebral region and became progressively smaller toward the tail. Large, irregularly arranged scales scattered along the dorsal surfaces from below the eyelids to the tail base and onto the limbs were grayish white. The dorsal ground color of the tail was yellowish gray, with nine irregular brown crossbands bordered by indistinct dark brown scales. The dorsal surfaces of the limbs were yellowish gray to yellowish brown, becoming reddish toward the toes.

Ventrally, the entire body was predominantly yellow, with the head being particularly bright reddish yellow. The ground color on the ventral surface of the head was reddish yellow, whereas that of the body, limbs, and tail was pale golden yellow. Sparse, irregular, and narrow grayish-brown patches occurred along both sides of the ventral surfaces of the body and limbs, as well as at the base of the tail.

Coloration of the holotype in preservation. In preservative (Fig. 4), the ground color on the dorsal surfaces of the head, body, and limbs turned gray. The eight indistinct pale yellowish-brown rounded blotches on the dorsum became slightly obscured, and the nine irregular brown crossbands on the tail also became more indistinct.

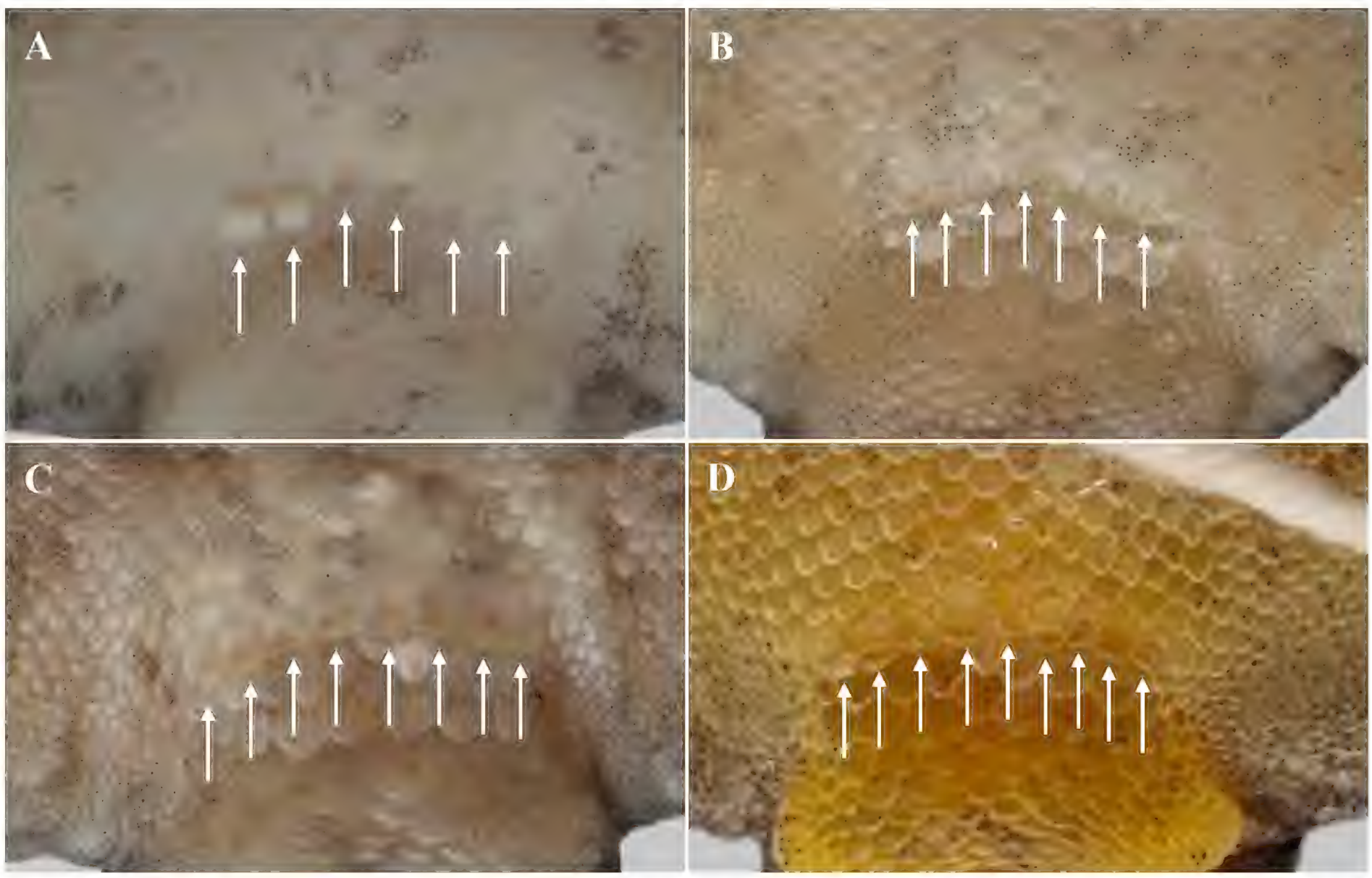

Figure 5. Precloacal pores in the adult male *Gekko asahi* sp. nov. **A.** Specimen SPMN-HP 003810, holotype; **B.** Specimen SPMN-HP 003812, paratype; **C.** Specimen SPMN-HP 003813, paratype; **D.** Specimen TMR-190. Photographs by T. Matsukoji.

The ventral surfaces faded to an ivory color, and the grayish-brown patches along the ventral body, limbs, and tail base faded to a pale grayish-brown.

Variation. The main morphological characters of *Gekko asahi* sp. nov. are summarized in Suppl. material 1: table S6. The species exhibits no evident sexual dimorphism in morphometric ratios, scale counts, or coloration. The longest known male measures SVL 73.85 mm (TMR-86); and the female measures SVL 73.96 mm (SPMN-HP 003811). SPL 7–9, IFL 6–9; large and slender towards the tip. IS absent; almost the same size. PO 14–18; preorbital region deeply concave. PM 2; common to all individuals. IOS 34–44; large towards the eyelids. Dorsal scales smooth, round to oval, granular and juxtaposed, SMC 158–189, SR 127–158. LRT 12–16; tubercles irregularly arranged, extending from the posterior part of the head to the anterior part of the tail, especially head has tubercles on the side surface of the head behind the eyes. PVT 17–23; present on dorsal surfaces. VS 32–45; venter slightly larger than dorsum, smooth, imbricate, and largest in middle of belly; precloacal scales enlarged, but no enlarged scales on thighs. PP 6–9 in males (Fig. 5), situated at the distal of each scale; PP absent in females. PAT one on each side, with the midpoint of the tubercle distinctly concave in some male individuals; in females, the postcloacal tubercles are smaller and less distinct. Dorsal scales of tail flat and smooth, irregular in size, with a few tubercles present on the anterior part of the tail; subcaudals small at the base, distinctly enlarged beyond the swollen portion, and arranged in a longitudinal row.

Forelimbs and hindlimbs well-developed; dorsal surface of the upper forelimb lacks tubercles, whereas the lower forelimb bears tubercles; the hindlimbs have tubercles across the entire dorsal surface. No webbing between the fingers and toes; digits moderately dilated; fingers and toes II–IV clawed; claws laterally compressed, extending beyond the terminal lamellae; LF1 8–11; LF4 9–14; LT1 9–12; LT4 10–18.

Main characters of the pattern in life (Fig. 6, 7). In life, the ground color on the dorsal surfaces of the head, body, limbs, and tail varies among individuals, ranging from gray to grayish brown, yellowish gray, yellowish brown, or dark brown. From the neck to the base of the tail, there are 8 to 9 indistinct pale yellowish-brown rounded blotches, and the tail bears 8 to 11 irregular brown crossbands bordered by indistinct dark brown scales. The ventral surfaces of the body are generally pale reddish yellow to pale yellowish-gold in life, and females tend to show a more vivid yellowish tint. In individuals with autotomized and regenerated tails, the regenerated portion is yellowish brown or brown, with numerous irregular brown or dark brown stripes.

Main characters of the pattern in preservation. In preservative, the coloration of the paratypes also resembled that of the holotype. The ground color on the dorsal surfaces of the head, body, limbs, and tail turned grayish white to gray. The indistinct pale yellowish-brown rounded blotches on the dorsum became further obscured, and the irregular brown crossbands on the tail also became more indistinct.

Distribution and ecology. *Gekko asahi* sp. nov. is currently known only from offshore islands and peninsulas of Nagasaki and Kagoshima Prefectures, Japan (Fig. 1, Suppl. material 1: Suppl. material 1: table S1). Its distribution includes the Hirado Islands (Hirado Island, Nakano-shima Island, Oitoku Island, Okinoshima Island, Toyaku Island); the Goto Islands (Fukue Island, Hisaka Island, Naru Island, Kaba Island, Mae Island, Kuro Island, Aka Island, Wakamatsu Island, Nakadori Island); the Danjyo Islands (Meshima Island, Oshima Island); Kuro Island; Enoshima Island; Oshima Island; Kakinoura Island; Matsu Island; Ohiki Island; Ike Island; and the Nishisonogi Peninsula in Nagasaki Prefecture. In Kagoshima Prefecture, the species occurs on the Koshiki Islands (Kami-Koshiki Island, Naka-Koshiki Island, Naka Island, Shimo-Koshiki Island), the Uji Islands, the Kusagaki Islands, and the Satsuma Peninsula (Morita 1987, 1988; Matsuo et al. 1988; Matsuo and Ejima 1988, 1989a, 1989b; Tokunaga 1988; Sengoku 1989; Shibata 1990; Matsuo 2019).

Sympatry has been recorded with *G. hokouensis* on Nakadori Island, Kami-Koshiki Island, Naka-Koshiki Island, and the Satsuma Peninsula (Matsuo 2019; Chiba and Chiba 2024), with *G. japonicus* on Hirado Island, Okinoshima Island, Fukue Island, Nakadori Island, Kakinoura Island, the Nishisonogi Peninsula, Kami-Koshiki Island, and the Satsuma Peninsula (Matsuo 2019; Chiba and Chiba 2024), and with *G. yakuensis* on the Satsuma Peninsula (Okamoto et al. 2025).

The species is nocturnal and inhabits primarily coastal rocky shores (Fig. 8), but also occurs on the walls of coastal buildings at elevations of 2–50 m asl. On inhabited islands where invasive geckos such as *Gekko japonicus* and *G. hokouensis* have not yet established, *Gekko asahi* sp. nov. is commonly observed both in rocky coastal areas and on nearby building walls. However, on uninhabited islands or inhabited islands where invasive geckos are established, it appears to prefer rocky coastal habitats exclusively (Chiba and Chiba 2024; see Discussion below). Females lay two eggs within rock crevices in relatively dry, sunlit sites during May and June (Matsuo 2005; Matsui and Mori 2021). Communal nesting is common, and numerous eggs may occur in a single crevice (Matsuo and Ejima 1988). Seasonal microhabitat preferences include sunny rocky areas in early spring, cool shaded crevices in midsummer, and deep rock crevices for overwintering (Matsuo 2005). The diet consists mainly of insects and wharf roaches, though predation on small mollusks has been reported (Matsui and Mori 2021). On the Koshiki Islands, multiple ant heads were detected in the feces of several individuals. In the wild, few individuals possess intact tails, and many have undergone autotomy at least once. Compared with its sister species *G. kaiyai*, which exhibits strong aggressiveness and rarely autotomizes its tail (Zhang et al. 2023), *Gekko asahi* sp. nov. may display tail autotomy more frequently.

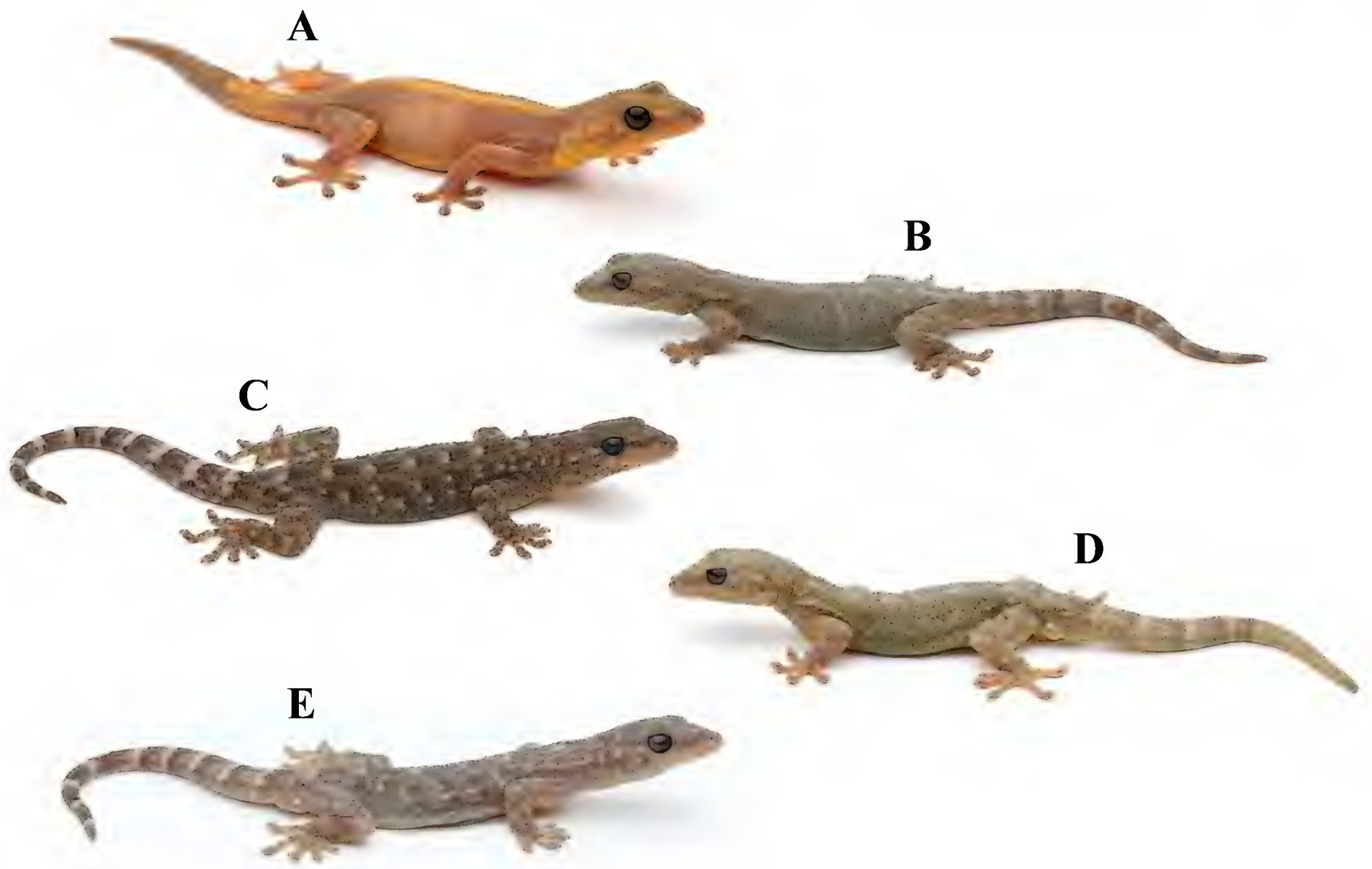

Figure 6. Coloration of *Gekko asahi* sp. nov. in life. **A.** Specimen TMR-208, adult female; **B.** Specimen TMR-96, adult female; **C.** Specimen SPMN-HP 003816, adult female, paratype; **D.** Specimen TMR-86, adult male; **E.** Specimen SPMN-HP 003813, adult male, paratype. Photographs by T. Matsukoji.

Comparisons. The main characteristics that distinguish *Gekko asahi* sp. nov. from other species of the subgenus *Japonigekko* are summarized in Table 2. Based on both morphological and molecular evidence, *Gekko asahi* sp. nov. is closely related to *G. kaiyai* and *G. hokouensis*. However, morphological comparisons and analyses revealed their differences (Fig. 3; Suppl. material 1: table S4). In particular, both males and females of *Gekko asahi* sp. nov. are significantly larger ($p < 0.05$) than those of *G. hokouensis* (mean SVL 64.4 ± 4.85, N = 12 in males; mean SVL 70.6 ± 5.43, N = 13 in females in *Gekko asahi* sp. nov. vs. mean SVL 55.1 ± 7.07, N = 3 in males; mean SVL 58.2 ± 4.43, N = 8 in females in *G. hokouensis*). Male *Gekko asahi* sp. nov. have greater HH/SVL (0.098 ± 0.007 vs. 0.087 ± 0.005) and FLL/SVL (0.122 ± 0.004 vs. 0.114 ± 0.008), but smaller IND/SVL (0.037 ± 0.002 vs. 0.042 ± 0.001) than in *G. hokouensis* (see Suppl. material 1: table S4). Female *Gekko asahi* sp. nov. have smaller HW/SVL (0.199 ± 0.004 vs. 0.206 ± 0.007) and EL/SVL (0.056 ± 0.003 vs. 0.064 ± 0.004) than in *G. hokouensis* (see Suppl. material 1: table S4).

Gekko asahi sp. nov. is also larger than *G. kaiyai* both in males (mean SVL 64.4 ± 4.85; N = 12 vs. 57.9 ± 4.09; N = 11) and females (mean SVL 70.6 ± 5.43; N = 13 vs. 62.0 ± 4.10; N = 4) (see Suppl. material 1: table S4). As compared to males of *G. kaiyai*, *Gekko asahi* sp. nov. males have greater SE/SVL (0.12 ± 0.003 vs. 0.08 ± 0.005) and EE/SVL (0.087 ± 0.005 vs. 0.075 ± 0.005), but smaller AG/SVL (0.43 ± 0.01 vs. 0.46 ± 0.02), HW/SVL (0.20 ± 0.005 vs. 0.22 ± 0.009), and HL/SVL (0.23 ± 0.01 vs. 0.26 ± 0.006). Females of *Gekko asahi* sp. nov. have smaller HW/SVL (0.19 ± 0.004 vs. 0.21 ± 0.007), but greater HH/SVL (0.096 ± 0.007 vs. 0.085 ± 0.008), SE/SVL (0.115 ± 0.005 vs. 0.077 ± 0.005), EE/SVL (0.084 ± 0.003 vs. 0.077 ± 0.004), and EL/SVL (0.056 ± 0.003 vs. 0.051 ± 0.002) than females of *G. kaiyai*.

In addition, *Gekko asahi* sp. nov. can be distinguished from *G. kaiyai* by having more SR (127–158 vs. 99–121), more IO (34–44 vs. 22–33); and in life, ventral surface of body pale reddish yellow, pale yellow, or pale yellowish-gold (vs. creamy white). And it can be distinguished from *G. hokouensis* by having fewer SPL (7–9 vs. 10–14), more IO (34–44 vs. 30–33), dorsal surfaces of both fore- and hindlimbs bearing tubercles (vs. lacking tubercles), and in life, ventral surface of body pale reddish yellow, pale yellow, or pale yellowish-gold (vs. creamy white).

In comparison with the other two sympatrically occurring species, *Gekko japonicus* and *G. yakuensis*, *Gekko asahi* sp. nov. can be distinguished from *G. japonicus* by having fewer PAT (1 vs. 3–5), dorsal surface of hindlimbs bearing tubercles (vs. lacking tubercles), and in life, ventral surface of body pale reddish yellow, pale yellow, or pale yellowish-gold (vs. creamy white). It can be further distinguished from *G. yakuensis* by having fewer SPL (7–9 vs. 12–13), and dorsal surfaces of both fore- and hindlimbs bearing tubercles (vs. lacking tubercles).

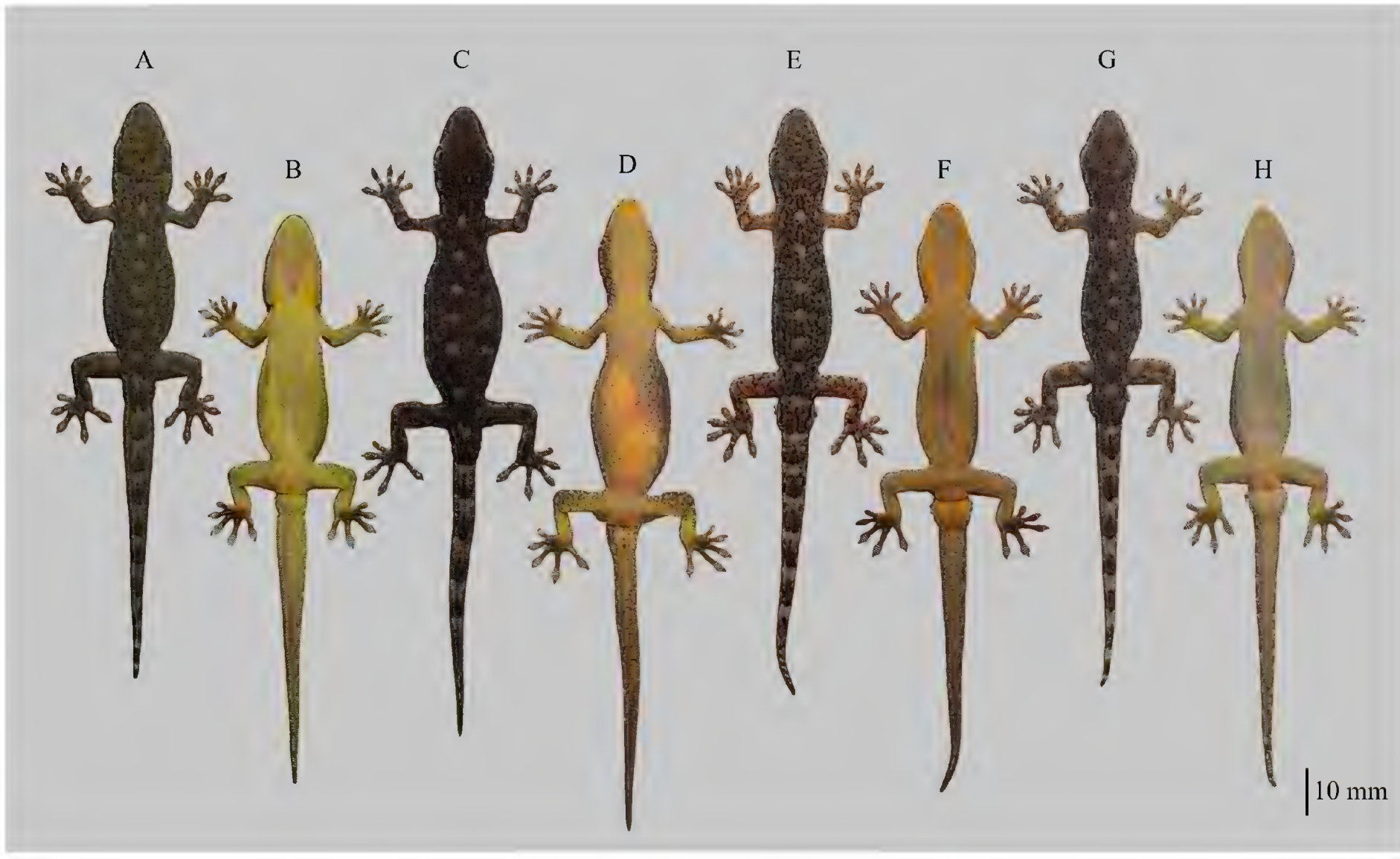

Figure 7. Fresh specimens of *Gekko asahi* sp. nov. **A, B.** Specimen TMR-66; **C, D.** Specimen TMR-197; **E, F.** Specimen TMR-180; **G, H.** Specimen SPMN-HP 003816. Photographs by T. Matsukoji.

By having SPL 7–9, *Gekko asahi* sp. nov. can be easily distinguished from *G. aaronbaueri* Tri, Thai, Phimvohan, David & Teynié, 2015, *G. adleri*, *G. bonkowskii* Luu, Calame, Nguyen, Le & Ziegler, 2015, *G. canhi* Rösler, Nguyen, Van Doan, Ho, Nguyen & Ziegler, 2010, *G. chinensis*, *G. cib*, *G. kwangsiensis* Yang, 2015, *G. liboensis* Zhou, Liu & Li, 1982, *G. liui* Zhou, Zhou, Wang, Li, Zhang, Li, Shen, Liu & Rao, 2025, *G. melli* Vogt, 1922, *G. nadenensis* Luu, Nguyen, Le, Bonkowski & Ziegler, 2017, *G. palmatus* Boulenger, 1907, *G. paucituberculatus* Wang, Qi, Zhou & Wang, 2024, *G. prep* Zhou, Chen, Liu, Li, Qi, Li & Peng, 2025, *G. scientiadventura* Rösler, Ziegler, Vu, Herrmann & Böhme, 2004, *G. shibatai* Toda, Sengoku, Hikida & Ota, 2008, *G. similignum*, *G. tesselatus* Xu, Ma, Cai, Qi, Matsukoji, Poyarkov, Sun, Jiang & Peng, 2025, *G. thakhekensis* Luu, Calame, Nguyen, Le, Bonkowski & Ziegler, 2014, *G. truongi* Phung & Ziegler, 2011, *G. vertebralis* Toda, Sengoku, Hikida & Ota, 2008, and *G. wenxianensis* Zhou & Wang, 2008, (vs. 13–14 in *G. aaronbaueri*, 10–15 in *G. adleri*, 12–14 in *G. bonkowskii*, 14 in *G. canhi*, 10–14 in *G. chinensis*, 10–12 in *G. cib*, 10–12 in *G. kwangsiensis*, 11 in *G. liboensis*, 11–13 in *G. liui*, 10–13 in *G. melli*, 12–14 in *G. nadenensis*, 11–15 in *G. palmatus*, 11 in *G. paucituberculatus*, 14 in *G. prep*, 12–14 in *G. scientiadventura*, 10–13 in *G. shibatai*, 12–14 in *G. similignum*, 10 or 11 in *G. tesselatus*, 12–14 in *G. thakhekensis*, 13–15 in *G. truongi*, 10–15 in *G. vertebralis*, and 12 in *G. wenxianensis*).

In addition, by having IO 34–44, *Gekko asahi* sp. nov. can be easily distinguished from *G. alpinus* Ma, Shi, Shen, Chang & Jiang, 2024, *G. auriverrucosus* Zhou & Liu, 1982, *G. fengshanensis* Huang, Wang, Qi, Song, Huang, Wang & Mo, 2025, *G. jinjiangensis* Hou, Shi, Wang, Shu, Zheng, Qi, Liu, Jiang & Xie, 2021, *G. khunkhamensis* Sitthivong, Lo, Nguyen, Ngo, Khotpathoom, Le, Ziegler & Luu, 2021, *G. scabridus* Liu & Zhou, 1982, *G. sengchanthavongi* Luu, Calame, Nguyen, Le & Ziegler, 2015, *G. swinhonis*, *G. taibaiensis* Song, 1985, and *G. tawaensis* (vs. 22–28 in *G. alpinus*, 26–27 in *G. auriverrucosus*, 22–27 in *G. fengshanensis*, 20–24 in *G. jinjiangensis*, 31–32 in *G. khunkhamensis*, 30 in *G. scabridus*, 28–32 in *G. sengchanthavongi*, 23–24 in *G. swinhonis*, and 28 in *G. taibaiensis* and *G. tawaensis*).

Finally, by the absence of webbing between the fingers and toes, *Gekko asahi* sp. nov. can be easily distinguished from *G. guishanicus* Lin & Yao, 2016, *G. ichangensis* Cao, Sucharitakul, Tie, Suwannapoom, Yan & Chomdej, 2025 and *G. subpalmatus* Günther, 1864 (vs. webbing present).

Discussion

Although *Gekko asahi* sp. nov. has remained undescribed until the present work, its natural history, ecological characteristics, and phylogenetic relationships had already been partly clarified by previous studies (Matsuo et al. 1988; Matsuo and Ejima 1988; Matsuo 2005; Matsui and Mori 2021; Chiba and Chiba 2024; Okamoto et al. 2025). Molecular phylogenetic analyses carried out in the present study recovered *Gekko*

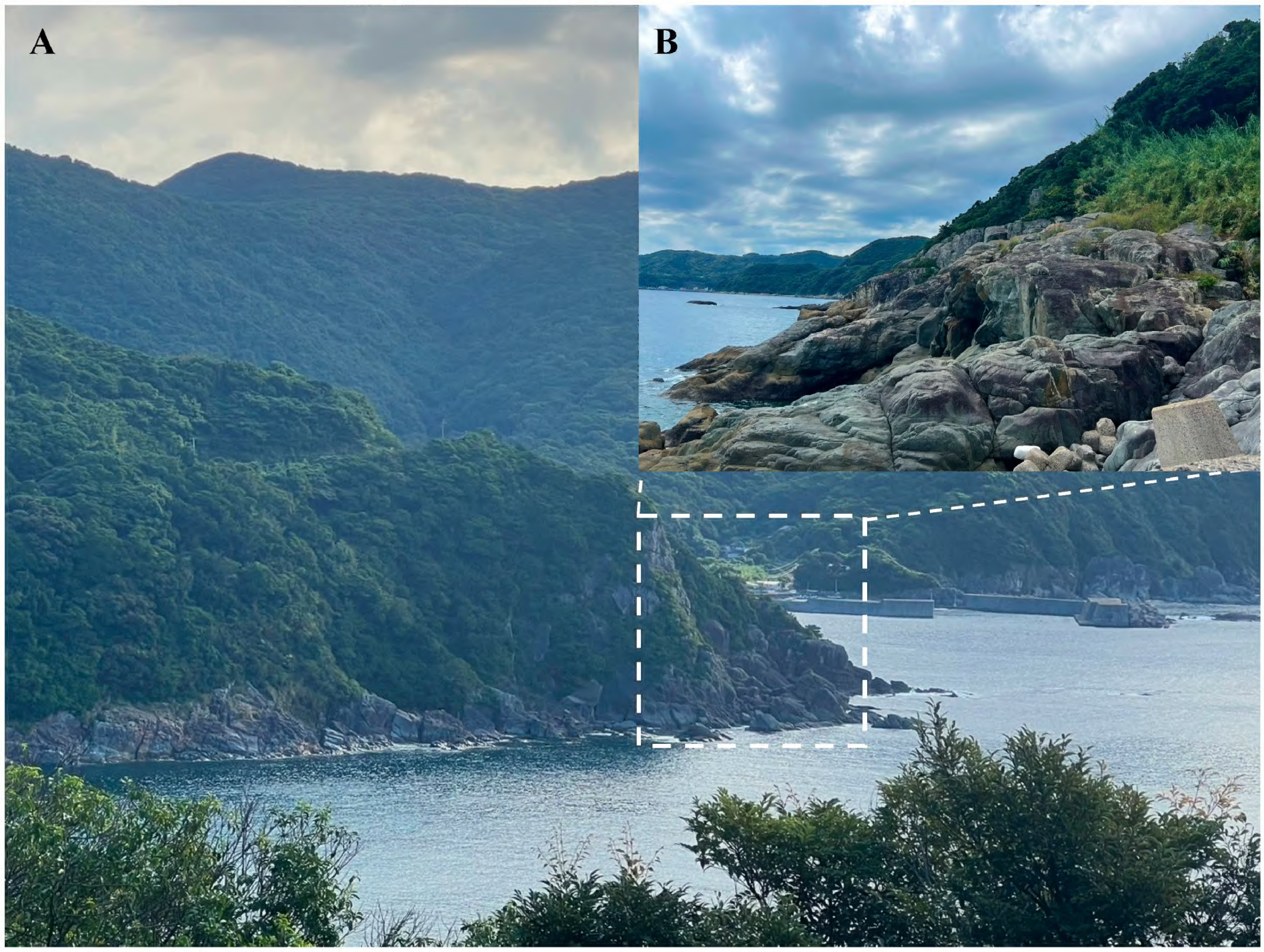

Figure 8. Habitat and field observations of *Gekko asahi* sp. nov. **A.** Macrohabitat of the new species in Nakadori Island, Shinkamigoto Town, Nagasaki Prefecture, Japan; **B.** Microhabitat of the new species. Photographs by M. Tsujita.

asahi sp. nov. as a strongly supported monophyletic lineage (SH = 100 / UFB = 100) within the subgenus *Japonigekko*. This lineage is subsequently recovered as the sister group to *G. kaiyai*, although with relatively low support (SH = 60 / UFB = 78). This topology, however, got a strong node support (ML BS 100 / BI PP 1.0) in the recent multilocus phylogenetic study of Cao et al. (2026), therefore, *Gekko asahi* sp. nov. indeed represents a sister species of *G. kaiyai*, which is currently known only from the Dabie Mountain region of Henan Province, central China. In contrast, *Gekko asahi* sp. nov. is restricted to Gotō Nada and the Nishisonogi Peninsula in Nagasaki Prefecture, as well as offshore islands of Kagoshima and the Satsuma Peninsula in Kagoshima Prefecture, Japan. The two species are separated by a vast geographic distance and are further isolated by extensive mountain systems and the intervening sea. This pronounced disjunction indicates long-term geographic isolation and supports the conclusion that *Gekko asahi* sp. nov. and *G. kaiyai* have followed independent evolutionary trajectories. It provides further evidence for the biogeographic hypothesis for the *Japonigekko* by Cao et al. (2026) which suggested the origin of this subgenus in Indochina with subsequent diversification in mainland China and numerous dispersal events from the mainland to the East Asian islands, including the Japanese Archipelago.

Ecological niche analyses from previous studies, comparing competitive and non-competitive regions in the Goto Islands, Koshiki Islands, and southern mainland Kyushu, revealed that the native gecko, *Gekko asahi* sp. nov., shows habitat preferences highly similar to those of the invasive congeners *Gekko japonicus* and *G. hokouensis*. In areas lacking invasive species, it predominantly occupies urban artificial habitats, whereas in regions of sympatry it tends to utilize natural environments, indicating that competitive interactions may shape its microhabitat use (Chiba and Chiba 2024).

Divergence-time estimation further indicated that populations on the Goto and Koshiki Islands diverged very recently, approximately 11,000 years ago, while those on Kami-Koshiki and Shimo-Koshiki Islands diverged only around 500 years ago (Chiba and Chiba 2024). Phylogenetic analyses based on mitochondrial (*tRNA-Phe-ND1*, 2900 bp) and partial nuclear *RAG-1* sequences placed *Gekko asahi* sp. nov. as the sister lineage to a clade including *G. vertebralis*, *G. tawaensis*, *G. hokouensis*, and *G. yakuensis* (Okamoto et al. 2025). Population-genetic analyses also revealed hybridization with introduced *G. japonicus* and *G. hokouensis* in parts

of southern Kyushu, as well as gene flow with the native *G. hokouensis* and *G. yakuensis* (Okamoto et al. 2025). Nevertheless, because most populations of this species inhabit island systems, such introgression appears geographically restricted. Across many islands in its native distribution, no evidence of gene flow with other congeners has been detected, supporting long-term isolation and reinforcing its recognition as a distinct evolutionary lineage.

In addition, this study provides the first publicly available *16S* and *ND2* sequences of *Gekko tawaensis* and incorporates them into a comprehensive phylogenetic analysis of the subgenus *Japonigekko*. An intriguing result is that *G. tawaensis* and *G. cib* form a strongly supported sister relationship (SH = 100 / UFB = 100), and the genetic divergence between them is extremely low: 2.2% in *16S*, comparable to the previously recognized minimum interspecific distance within the subgenus, and 3.3% in *ND2*, which is substantially lower than the formerly known minimum of 5.4% between *G. chinensis* and *G. similignum*. This pattern is inconsistent with their distinct biogeographic contexts, as the two species inhabit geographically and ecologically different regions. A plausible explanation is that one of the taxa may have been introduced by human activities, followed by limited subsequent evolutionary divergence. To clarify their true taxonomic status and dispersal history, future work should involve broad-scale intensive sampling combined with high-depth genomic sequencing, which will be essential for evaluating species boundaries, reconstructing dispersal pathways, and determining whether artificial translocation has played a role in shaping their current distributions.

The discovery of *Gekko asahi* sp. nov. increases the number of known species in the subgenus *Japonigekko* to 40, and raises the number of species recorded from Japan to 7. This finding demonstrates that the survey and documentation of amphibian and reptile diversity in islands of Kyushu District remain insufficient. In future studies we aim to clarify the genetic population structure of this species by including populations from numerous uninhabited islands that could not be surveyed in our analysis.

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References

Akaike H (1973) Information theory and an extension of the maximum likelihood principle. In: Petrov BN, Csáki F (Eds) Second International Symposium on Information Theory, Tsahkadsor, Armenia, USSR. Akadémiai Kiadó, Budapest, 267–281.

Akaike H (1974) A new look at the statistical model identification. IEEE Transactions on Automatic Control 19(6): 716–723.

Burland TG (2000) DNASTAR's Lasergene sequence analysis software. Methods Molecular Biology 132: 71–91. https://doi.org/10.1385/1-59259-192-2:71

Cao J, Sucharitakul P, Tie M, Suwannapoom C, Yan F, Chomdej S (2025) A new species of the genus *Gekko* Laurenti, 1768 (Squamata: Gekkonidae) from Hubei, China. Asian Herpetological Research 16(1): 110–121. https://doi.org/10.3724/ahr.2095-0357.2024.0046

Cao J, Poyarkov NA, Wei P, Tie M, Matsukoji T, Suwannapoom C, Ai R, Lu W, Sucharitakul P, Wang H, Chomdej S, Yuan Z, Yan F (2026) Diversity, phylogeny, and biogeography of the subgenus *Japonigekko* (Gekkonidae: Gekko). Molecular Phylogenetics and Evolution 217: 108530 (1–11). https://doi.org/10.1016/j.ympev.2025.108530

Chiba M, Chiba S (2024) Hidden invasiveness of non-native Schlegel's Japanese gecko (Reptilia: Squamata: Gekkonidae) and three-way competition among natives and non-natives in Japan. Molecular Ecology 33: 1–14. https://doi.org/10.1111/mec.17420

Edgar RC (2004) MUSCLE: Multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Research 32(5): 1792–1797. https://doi.org/10.1093/nar/gkh340

Hillis DM, Moritz C, Mable BK (1996) Molecular systematics. Sinauer, Sunderland, Massachusetts, 655 pp. https://doi.org/10.2307/1447682

Hoang DT, Chernomor O, Haeseler AV, Minh BQ, Vinh LS (2018) UFBoot2: Improving the ultrafast bootstrap approximation. Molecular Biology and Evolution 35(2): 518–522. https://doi.org/10.1093/molbev/msx281

Hou YM, Shi SC, Wang G, Shu GC, Zheng PY, Qi Y, Liu GH, Jiang JP, Xie F (2021) A New species of the *Gekko japonicus* group (Squamata: Gekkonidae) from southwest China. Asian Herpetological Research 12: 36–48. https://doi.org/10.16373/j.cnki.ahr.200064

Huang Z, Wang HT, Qi S, Song HM, Huang Y, Wang YY, Mo YM (2025) A new species of karst-adapted gecko (Squamata: Gekkonidae: *Gekko*) from Guangxi, southern China. ZooKeys 1245: 289–310. https://doi.org/10.3897/zookeys.1245.153769

Jonniaux P, Kumazawa Y (2008) Molecular phylogenetic and dating analyses using mitochondrial DNA sequences of eyelid geckos (Squamata: Eublepharidae). Gene 407(1–2): 105–115. https://doi.org/10.1016/j.gene.2007.09.023

Jono T (2016) Absence of temporal pattern in courtship signals suggests loss of species recognition in gecko lizards. Evolutionary Ecology 30(4): 583–600.

Kalyaanamoorthy S, Minh BQ, Wong TKF, Haeseler AV, Jermiin LS (2017) ModelFinder: fast model selection for accurate phylogenetic estimates. Nature Methods 14(6): 587–589. https://doi.org/10.1038/nmeth.4285

Kumar S, Stecher G, Li M, Knyaz C, Tamura K (2018) MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. Molecular Biology and Evolution 35: 1547–1549. https://doi.org/10.1093/molbev/msy096

Lin JT, Yao CJ (2016) A new species of the genus *Gekko* (Squamata: Sauria: Gekkonidae) from Guishan Isle, Yilan County, Taiwan.

Journal of the National Taiwan Museum 69: 1–14. https://doi.org/10.6532/JNTM.2016.69(2).01 [in Chinese]

Luu VQ, Calame T, Nguyen TQ, Le MD, Bonkowski M, Ziegler T (2014) A new species of the *Gekko japonicus* group (Squamata: Gekkonidae) from central Laos. Zootaxa 3895(1): 73–88. https://doi.org/10.11646/zootaxa.3895.1.4

Luu VQ, Calame T, Nguyen TQ, Le MD, Ziegler T (2015) Morphological and molecular review of the *Gekko* diversity of Laos with descriptions of three new species. Zootaxa 3986(3): 279–306. https://doi.org/10.11646/zootaxa.3986.3.2

Luu VQ, Nguyen TQ, Le MD, Bonkowski M, Ziegler T (2017) A new karst dwelling species of the *Gekko japonicus* group (Squamata: Gekkonidae) from central Laos. Zootaxa 4263(1): 179–193. https://doi.org/10.11646/zootaxa.4263.1.10

Lyu ZT, Lin CY, Ren JL, Jiang K, Zhang YP, Qi S, Wang J (2021) Review of the *Gekko* (*Japonigekko*) *subpalmatus* complex (Squamata, Sauria, Gekkonidae), with description of a new species from China. Zootaxa 4951(2): 236–258. https://doi.org/10.11646/zootaxa.4951.2.2

Matsui M, Mori A, Editors-in-Chief (2021) Amphibians and Reptiles of Japan. Herpetological Society of Japan, 122 pp.

Matsuo T, Ejima M, Matsunaga K (1988) A species of gecko belonging to genus *Gekko* in Nakadori-jima Island, Gotō Islands. Nihon no Seibutsu (The Natural History of Japan) 2(2): 61.

Matsuo T, Ejima M (1988) New locality for a species of genus *Gekko* in Nagasaki Prefecture. Nihon no Seibutsu (The Natural History of Japan) 2(12): 56–58.

Matsuo T, Ejima M (1989a) Ecology of the Nishi-yamori on the Danjyo Islands. Nihon no Seibutsu (The Natural History of Japan) 3(12): 44–46.

Matsuo T, Ejima M (1989b) Nishi-yamori of mainland Nagasaki Prefecture. Nihon no Seibutsu (The Natural History of Japan) 4(1): 77.

Matsuo T (2005) Amphibians and Reptiles of Nagasaki Prefecture. Nagasakishinbunsya, 155 pp.

Matsuo T (2019) Four Species of *Gekko* in Nagasaki Prefecture. Trans. Nagasaki Biology Society 84: 33–37. https://nagasaki-u.repo.nii.ac.jp [in Japanese]

Ma S, Shi SC, Shen C, Chang LM, Jiang JP (2024) Discovery of a new species of the subgenus *Japonigekko* (Squamata: Gekkonidae: *Gekko*) from the Hengduan Mountains, southwestern China: the best *Japonigekko* mountaineer. ZooKeys 1215: 289–309. https://doi.org/10.3897/zookeys.1215.125043

Ministry of the Environment of Japan (2025) Ecologically or Biologically Significant marine Areas identified by Japan. https://www.env.go.jp/nature/biodic/kaiyo-hozen/kaiiki/engan/15501.html [accessed 27 November 2025]

Morita T (1987) Visiting the Animals of the Uji Islands. Kagoshimaken Koutougakkou Kyouikukenkyukai Rikabukaishi (28): 27–38.

Morita T (1988) Terrestrial Vertebrate Fauna of Kuro Island. Kagoshimaken Koutougakkou Kyouikukenkyukai Rikabukaishi 29: 12–20.

Ngo VT, Pham TH, Phimvohan A, David P, Teynié A (2015) *Gekko aaronbaueri*, a new gecko (Squamata: Gekkonidae) from central Laos. Zootaxa 3914(2): 144–156. https://doi.org/10.11646/zootaxa.3914.2.4

Nguyen LT, Schmidt HA, Haeseler AV, Minh BQ (2015) IQ-TREE: A fast and effective stochastic algorithm for estimating maximum likelihood phylogenies. Molecular Biology and Evolution 32(1): 268–274. https://doi.org/10.1093/molbev/msu300

Nguyen TQ, Wang YY, Yang JH, Lehmann T, Le MD, Ziegler T, Bonkowski M (2013) A new species of the *Gekko japonicus* group (Squamata: Sauria: Gekkonidae) from the border region between China and Vietnam. Zootaxa 3652: 501–518. https://doi.org/10.11646/zootaxa.3652.5.1

Nishikawa K, Matsui M, Tanabe S, Sato SI (2007) Morphological and allozymic variation in *Hynobius boulengeri* and *H. stejnegeri* (Amphibia: Urodela: Hynobiidae). Zoological Science 24: 752–766. https://doi.org/10.2108/zsj.24.752

Ota H, Lau MW, Weidenhöfer T, Yasukawa Y, Bogadek A (1995) Taxonomic review of the geckos allied to *Gekko chinensis* Gray 1842 (Gekkonidae Reptilia) from China and Vietnam. Tropical Zoology 8(1): 181–196. https://doi.org/10.1080/03946975.1995.10539278

Okamoto K, Toda M (2022) Distribution of the Gekko spp. in Kagoshima Prefecture and hybridizations in their contact zorns. Kyushu Herpetological Society 13: 53–59.

Okamoto K, Jono T, Tanioka H, Sueyoshi T, Matsuo T, Toda M (2025) Natural hybridization among species of the genus *Gekko* (Squamata: Gekkonidae) in Japan: the roles of pre- and postmating isolation. Zoologischer Anzeiger 319: 196–209. https://doi.org/10.1016/j.jcz.2025.09.008

Pauwels OSG, Meesook W, Donbundit N, Jindamad T, Topai N, Sumontha M (2025) Gekko (Gekko) shiva, a new limestone-dwelling gecko from Sa Kaeo Province, eastern Thailand (Squamata, Gekkonidae). Zootaxa 5588(2): 305–322. https://doi.org/10.11646/zootaxa.5588.2.6

Phung TM, Ziegler T (2011) Another new *Gekko* species (Squamata: Gekkonidae) from southern Vietnam. Zootaxa 3129: 51–61. https://doi.org/10.11646/zootaxa.3129.1.4

Rambaut A (2018) FigTree v1.4.4. http://tree.bio.ed.ac.uk/software/figtree/ [accessed 10 April 2025]

Rösler H, Bauer AM, Heinicke MP, Greenbaum E, Jackman T, Nguyen TQ, Ziegler T (2011) Phylogeny, taxonomy, and zoogeography of the genus *Gekko* Laurenti, 1768 with the revalidation of *G. reevesii* Gray, 1831 (Sauria: Gekkonidae). Zootaxa 2989: 1–50. https://doi.org/10.11646/zootaxa.2989.1.1

Rösler H, Ziegler T, Vu NT, Herrmann HW, Böhme W (2005 [2004]) A new lizard of the genus *Gekko* Laurenti, 1768 (Squamata: Sauria: Gekkonidae) from the Phong Nha-Ke Bang National Park, Quang Binh Province, Vietnam. Bonner zoologische Beiträge 53: 135–148.

Sengoku S (1989) Notes on a *Gekko* population in the Danjo Group, Nagasaki Prefecture, Japan. In: Matsui M, Hikida T, Goris RC (Eds) Current Herpetology in East Asia. Herpetological Society of Japan, Kyoto: 180–184.

Shibata Y (1990) *Gekko* sp. from the Koshiki Islands, Kyushu, Japan (Reptilia: Gekkonidae). Osaka Museum of Natural History 2: 77–82. https://www.omnh.jp [in Japanese]

Simon C, Frati F, Beckenbach A, Crespi B, Liu H, Flook P (1994) Evolution, weighting, and phylogenetic utility of mitochondrial gene sequences and a compilation of conserved polymerase chain reaction primers. Annals of the Entomological Society of America 87(6): 651–701. https://doi.org/10.1093/aesa/87.6.651

Sitthivong S, Lo OV, Nguyen TQ, Ngo HT, Khotpathoom T, Le MD, Ziegler T, Luu VQ (2021) A new species of the *Gekko japonicus* group (Squamata: Gekkonidae) from Khammouane Province, central Laos. Zootaxa 5082(6): 553–571. https://doi.org/10.11646/zootaxa.5082.6.3

Song HM, Wang HT, Lin ZH, Zheng SS, Zhou ZE, Gong YN, Liu ZF, Li YY, Qi S, Wang YY (2024) Eight new records of amphibians and reptiles in Guangdong Province, China. Chinese Journal of Zoology, 59(5): 658–686. https://doi.org/10.13859/j.cjz.202424014 [in Chinese]

Song MT (1985) A new species of *Gekko* from Shaanxi. Acta Herpetologica Sinica 4: 329–330. [in Chinese]

Stejneger L (1907) Herpetology of Japan and adjacent territory. Bulletin of the United States National Museum 58: 165–169. https://doi.org/10.5479/si.03629236.58.i

StatSoft INC (2001) STATISTICA (data analysis software system), version 6. Tulsa, OK, 91–94.

Stephane G, Jean-franc OD, Vincent L, Maria A, Wim H, And OG (2010) New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Systematic Biology 59(3): 307–321. https://doi.org/10.1093/sysbio/syq010

Toda M, Sengoku S, Hikida T, Ota H (2008) Description of two new species of the genus *Gekko* (Squamata: Gekkonidae) from the Tokara and Amami Island Groups in the Ryukyu Archipelago, Japan. Copeia 2008: 452–466. https://doi.org/10.1643/CH-06-281

Tokunaga S (1988) A gecko of the genus *Gekko* from Taka-shima Island, Hirado, Nagasaki, Japan (Reptilia: Lacertilia). Japanese Journal of Herpetology 12: 127–130.

Uetz P, Freed P, Aguilar R, Reyes F, Hošek J (2025) The Reptile Database. http://www.reptile-database.org [accessed 27 November 2025]

Wang HT, Qi S, Zhou DY, Wang YY (2024) Description of a new karst-adapted species of the subgenus *Japonigekko* (Squamata: Gekkonidae: *Gekko*) from Guangxi, southern China. Vertebrate Zoology 74: 121–132. https://doi.org/10.3897/vz.74.e113899

Wood Jr PL, Guo X, Travers SL, Su Y, Olson KV, Bauer AM, Grismer LL, Siler CD, Moyle RG, Andersen MJ, Brown RM (2020) Parachute gecko free fall into synonymy: Gekko phylogeny, and a new subgeneric classification, inferred from thousands of ultraconserved elements. Molecular Phylogenetics and Evolution 146: 106731. https://doi.org/10.1016/j.ympev.2020.106731

Xu Y, Ma S, Cai B, Qi S, Matsukoji T, Poyarkov NA, Sun F, Weng S, Gu T, Tian K, Zhang D, Jiang J, Peng L (2025) A new rock-dwelling gecko of the subgenus *Japonigekko* (Squamata: Gekkonidae: *Gekko*) from northwestern Sichuan Province, China. Zoosystematics and Evolution 101(4): 2221–2242. https://doi.org/10.3897/zse.101.175246

Yang JH (2015) A new species of the genus *Gekko* Laurenti (Squamata: Sauria: Gekkonidae) from Guangxi, China. Zootaxa 3936(2): 287–295. https://doi.org/10.11646/zootaxa.3936.2.9

Zhang CW, Wu AF, Cai B, Wang LR, Pang DP, Ma HH, Yu L, Li XY, Huang H, Zeng L, Li L, Yan J, Li P, Zhang BW (2023) A New Species of the Genus *Gekko* (Squamata: Sauria: Gekkonidae) from the Dabie Mountains, China. Animals 13(24): 3796. https://doi.org/10.3390/ani13243796

Zhang D, Gao FL, Jakovlić I, Zou H, Zhang J, Li WX, Wang GT (2020) PhyloSuite: an integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. Molecular Ecology Resources 20(1): 348–355. https://doi.org/10.1111/1755-0998.13096

Zhao E, Zhao K, Zhou K (1999) Fauna Sinica Reptilia, Vol. 2: Squamata, Lacertilia. Science Press, Beijing, [xi +] 394 pp. [in Chinese]

Zhou K, Wang Q (2008) New species of *Gekko* (Squamata: Sauria: Gekkonidae) from China: morphological and molecular evidence. Zootaxa 1778(1): 59–68. https://doi.org/10.11646/zootaxa.1778.1.5

Zhou KY, Liu YZ, Li DJ (1982) Three new species of *Gekko* and remarks on *Gekko hokouensis* (Lacertiformes, Gekkonidae). Acta Zootaxonomica Sinica 7: 438–446. [in Chinese]

Zhou KY, Li HD, Han DM, Bauer AM, Feng JY (2006) The complete mitochondrial genome of *Gekko gecko* (Reptilia: Gekkonidae) and support for the monophyly of Sauria including Amphisbaenia. Molecular Phylogenetics and Evolution 40(3): 887–892. https://doi.org/10.1016/j.ympev.2006.04.003

Zhou RB, Chen KZ, Liu QM, Li XJ, Qi XM, Li JL, Peng XP (2025a) Description of a new species of the subgenus *Japonigekko* (Squamata: Gekkonidae: *Gekko*) from Hainan, China. Zootaxa 5633(3): 528–540. https://doi.org/10.11646/zootaxa.5633.3.6

Zhou RB, Zhou HX, Wang HS, Li J, Zhang DR, Li XY, Shen ZQ, Liu S, Rao DQ (2025b) Taxonomic review of *Gekko* (*Japonigekko*) species in Hainan Province and description of a new species. Asian Herpetological Research 16(2): 247–259. https://doi.org/10.3724/ahr.2095-0357.2024.0055

Supplementary material 1

Additional information

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Data type: zip

Explanation note: **table S1.** Verified localities of *Gekko asahi* sp. nov. used to generate the map in Fig. 1. These localities were based on vouchered material and literature records. **table S2.** Uncorrected *p*-distances (%) of the *ND2* gene among species of *Japonigekko* used in this study. "/" indicates not available. **table S3.** Uncorrected *p*-distances (%) of the *16S* gene among species of *Japonigekko* used in this study. "/" indicates not available. **table S4.** Resulting p values from univariate morphological analyses comparing the geographic populations of *Gekko* sp. from the Koshiki Islands, *G. hokouensis* and *G. kaiyai*. Characters in bold (marked in red) are considered statistically significant. All characters were examined using Student's T Tests. **table S5.** Variable contributions based on correlations and statistics for the Principal Components Analysis (PCA) consisting of members of the *Gekko hokouensis* clade. Abbreviations are listed in the materials and methods. **table S6.** Morphological dataset of *Gekko asahi* sp. nov. based on the examined specimens. See Materials and Methods for abbreviations of morphological characters.

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